

HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S. Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE ENCODING THE SAME to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct
5 signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit
10 specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis,
15 carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to
20 activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding α subunit, a β subunit, and a γ subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the α subunit. When GDP is bound, the G protein exists as a heterotrimer: the $G\alpha\beta\gamma$ complex. When GTP is bound, the α subunit dissociates from the heterotrimer, leaving a $G\beta\gamma$ complex. When
25 a $G\alpha\beta\gamma$ complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound $G\alpha$ subunit from the $G\alpha\beta\gamma$ complex increases. The free $G\alpha$ subunit and $G\beta\gamma$ complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form
30 the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby

suggesting a possible role of ORs in sperm chemotaxis (Parmenthien, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204, SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

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NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

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NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO.
279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287,
5 SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ.
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SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ.
10 ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID.
NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO.
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15 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381,
SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ.
ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID.
NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO.
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20 SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ.
ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID.
NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO.
441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449,
SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ.
25 ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID.
NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO.
475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483,
SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ.
ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO:
30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and
SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100,
or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ.
10 ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61,
15 SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID.
20 NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.
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30 NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.

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NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.
243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251,
5 SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ.
ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID.
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10 ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID.
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311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319,
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ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID.
15 NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO.
345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353,
SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ.
ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO:
371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379,
20 SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ.
ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID.
NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO.
405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413,
SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ.
25 ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID.
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ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID.
30 NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO.
473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481,
SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ.
ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO: 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60, 80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and
5 quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the
10 perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of
15 molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception
20 in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a
25 predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising:
30 a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provide a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments or variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4 n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n ORs of said vertebrate, where n is greater than or equal to 4, n is greater than or equal to 12; n is greater than or equal to 24, n is greater than or equal to 48; n is greater than or equal to 72; n is greater than or equal to 96; n is greater than or equal to 120; n is greater than or equal to 144; n is greater than or equal to 168; n is greater than or equal to 192; n is greater than or equal to 216, or n is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

Brief Description of the Drawings

5 Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

 Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

 Figure 3 illustrates the multiple sequence alignment derived for fifty novel
20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the
25 AOLFR110 amino acid sequence.

 Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,

AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.*, Mistili *et al.*, *Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in Ca^{2+} levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular Ca^{2+} levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A⁺ RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

A. Identification and Characterization of Olfactory Receptors

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*; Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating
5 searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a
10 scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and
15 X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989))
20 alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-
25 called "tree" or "dendrogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of
30 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using
5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were
10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most
15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as
20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close
25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of
30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

B. Definitions

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP₃, cAMP, cGMP, and Ca²⁺ via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain,” “extracellular domains,” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

“Extracellular domains” therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the “N terminal domain” that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The “N terminal domain” region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. “Transmembrane domain,” which comprises the seven “transmembrane regions,” refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

“Cytoplasmic domains” refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the “C terminal domain” and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. “C terminal domain” refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm.

The term “ligand-binding region” or “ligand-binding domain” refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase “functional effects” in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, IP3, or intracellular Ca^{2+}), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By “determining the functional effect” in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

“Inhibitors,” “activators,” and “modulators” of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor

with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate
5 and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or
10 absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a
15 relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms “purified,” “substantially purified,” and “isolated” as used herein
20 refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the “purified,” “substantially purified,” and “isolated” subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the
25 compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms “purified,” “substantially purified,” and “isolated” “isolated,” when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or
30 concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5 As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or
10 compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the
15 art.

As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide
20 primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, tastant-binding sequences of the invention) *in vivo* or *in vitro*.

The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma
25 membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30 The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term “nucleic acid” or “nucleic acid sequence” refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded
5 form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata, *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev*, 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly
15 encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzner *et al.*, *Nucleic
20 Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms “polypeptide,” “peptide” and “protein” are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term “plasma membrane translocation domain” or simply “translocation domain” means a polypeptide domain that, when incorporated into the amino terminus
30 of a polypeptide coding sequence, can with great efficiency “chaperone” or “translocate” the hybrid (“fusion”) protein to the cell plasma membrane. For instance, a “translocation domain” may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (e.g., an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

10 “Functional equivalency” means the domain’s ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relatively efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

15 The “translocation domain,” “ligand-binding domain”, and chimeric receptors compositions described herein also include “analogs,” or “conservative variants” and “mimetics” (“peptidomimetics”) with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (e.g., acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids
5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only
15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative
20 substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that
25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.,* Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*
30 *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

5 The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can
10 also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the
15 invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues
20 which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or
25 coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH₂- for -C(=O)-NH-), aminomethylene (CH₂-NH), ethylene, olefin
30 (CH=CH), ether (CH₂-O), thioether (CH₂-S), tetrazole (CN₄), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

5 A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter
10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the
15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other
20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the
25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer

sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (*e.g.*, 10 to 50 nucleotides) and at least about 60° C for long probes (*e.g.*, greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, *e.g.*, 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad
5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair
10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant
15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or
20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding
25 properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated
30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase “selectively associates with” refers to the ability of a nucleic acid to “selectively hybridize” with another as defined above, or the ability of an antibody to “selectively (or specifically) bind to a protein, as defined above.

The term “expression vector” refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression “cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By “host cell” is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g., cultured cells, explants, and cells in vivo.*

C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and
5 libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of
10 the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

15 The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or
20 plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.*
25 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand
30 using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I*,
5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid
10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-
15 PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned
20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y. (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain
25 reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwoh, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g.,
30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of
5 vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that,
10 when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises
15 substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues
20 that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of
25 olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through
30 VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g.,* Rose, *Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine, 3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using

degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, *e.g.*, olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art
5 (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (*see, e.g.*, Buiakova,
10 *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be
15 used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, *e.g.*, antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in
20 culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked
25 to transcriptional or translational control elements, *e.g.*, transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the
30 desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, *e.g.*, a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural
5 sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional
10 elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the
15 FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane
20 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate
25 detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g., Kroll, DNA Cell. Biol.* 12:441-53 (1993)).

30 Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (*see, e.g.*, Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g.*, episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g.*, chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (*e.g.*, chlorosulfuron or Basta) to permit selection of those cells transformed with the desired DNA sequences (*see, e.g.*, Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have similar primary sequences and secondary and tertiary structures, structural domains (*e.g.*, TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and “discover modeling”); <http://bioinfo.weizmann.ac.il/>.

5 The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of olfactory receptor ligand-binding TM domain sequences can
10 include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel
15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,
20 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another
25 G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the
30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein, β -gal, glutamate receptor, and the rhodopsin presequence.

Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, i.e., which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors, fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

D. Immunological Detection of OR Polypeptides

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

1. Antibodies to OR family members

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5 Monoclonal antibodies and polyclonal sera are collected and titered against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 109 or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other
10 organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a K_d of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

 Once OR family member specific antibodies are available, individual OR
15 proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, *see Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

20 2. Immunological binding assays

 OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (*see, e.g.*, U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, *see* also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);
25 *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (*e.g.*, anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30 Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the

labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol., 111:1401-1406 (1973); Akerstrom et al., J. Immunol., 135:2589-2542 (1985)*). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin.

10 A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

a. Non-competitive assay formats

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred “sandwich” assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

b. Competitive assay formats

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

c. Cross-reactivity determinations

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

5 The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding
10 of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

15 Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be make by subtracting out cross-reactive antibodies using
20 other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

d. Other assay formats

25 Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that
30 specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5 **e. Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific
10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

f. Labels

15 The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such
20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADSTM) (SEQ ID NO: 529), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, ³H, ¹²⁵I, ³⁵S, ¹⁴C,
25 or ³²P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety
30 of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecule (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

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Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.

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Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, e.g. the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked
5 to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises
10 all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in
15 vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For
20 example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by
25 looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the
30 activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP γ S assay may be used. As described above, upon activation of a GPCR, the G α subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP γ ³⁵S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP γ S are added to the assay, and binding of GTP γ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP γ S can be utilized.

2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand, it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

Where \parallel is the intensity of the emission light parallel to the excitation light plane and \perp is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon ® and Beacon 2000™ System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity (η), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

The rotational relaxation time is small (\approx 1 nanosecond) for small molecules (e.g. fluorescein) and large (\approx 100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules, dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory
30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals
5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody
10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,
15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D;
20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes,
25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about
30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, e.g., ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

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15 SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID
NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID
20 NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and
conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of
the protein, which encodes the structural information of the protein. At least 10
25 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino
acids) are entered into the computer system from computer keyboards, computer
readable substrates that include, but are not limited to, electronic storage media (*e.g.*,
magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM),
information distributed by internet sites, and by RAM. The three-dimensional
30 structural model of the protein is then generated by the interaction of the amino acid
sequence and the computer system, using software known to those of skill in the art. .

The amino acid sequence represents a primary structure that encodes the
information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as “energy terms,” and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then
10 formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of
20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.

- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

5. Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, e.g., G α 15, that is capable of coupling the chimeric receptor to an intracellular signaling pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of ^{32}P from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, see, e.g., *Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269-277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as Ca^{2+} , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed
5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G α 15 and G α 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,
10 increases in second messengers such as IP₃, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP₃) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP₃ in turn stimulates the release of intracellular calcium ion stores. Thus, a change in
15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP₃ can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in
20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are
25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents
30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G α 15/G α 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by
10 measuring changes in intracellular Ca²⁺ levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca²⁺ levels are optionally measured using fluorescent Ca²⁺ indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and
25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the
30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.,* Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

6. Transgenic non-human animals expressing olfactory receptors

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such

vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as
5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable
10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate
15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezeh, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*
20 *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal
25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type
30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a “knockout” cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, “gene trap insertion” can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene’s expression; or a combination thereof. Gene targeting via homologous recombination in pluripotent embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce “knockout” human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce “knock-ins” in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

F. Modulators

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to
5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka
10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As
15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such
20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a
30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

G. Methods for Representing and Predicting the Perception of Odor

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the
5 receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a
10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the
15 representation may constitute a point or a volume in n -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values X_1 to X_n representative of the quantitative stimulation of
20 each of n olfactory receptors of said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations
25 of molecules yielding known olfactory perception in a mammal, providing values X_1 to X_n representative of the quantitative stimulation of each of n olfactory receptors of
30 said vertebrate, where n is greater than or equal to 4, for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

25 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

H. Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

EXAMPLES

AOLFR1 sequences:

MKTFSSFLQIGRNMHQGNQTTITEFILLGFFKQDEHQNLLFVLFLGMYLVTVIGNGLIIVAISLD
TYLHTPMYFLANLSFADISSISNSVPKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLLGTM
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALHTLLLIQLLFCNHNTLPHFCDLAPLL
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCIIRAVLRVSSTQGKWKAFTCGSHLTVVLLFY
GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMNPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID
NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATATTGTGGCTA
TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTTCCTTGCCAATCTATCCTTTGCT
GATATTTCTCCATTTCCAACCTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC

AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCGTCATT
 GACAATTTGCTCTTGGGGACCATGGCCTATGACCACTTTGTGGCGATCTGCCACCCTCTGA
 ATTATACAATTCTCATGCGGCCAGGTTTCGGCATTGCTCACAGTCATCTCATGGTTCCTC
 AGTAATATTATTGCTCTGACACACACCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA
 5 CACTCTCCACACTTCTTCTGTGACTTGGCCCCCTCTGCTCAAACGTCTCTGTTTACAGATACAT
 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCCTTTACACTC
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCTGAGAGTATCTTCCACACAGGGAA
 AGTGGAAGGCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC
 CATTGTAGGCGTGTACTTTTCCCCTCTCCACTCACCTGAGGACACTGATAAGATTGGT
 10 GCTGTCTTATTCACTGTGGTGACCCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCCTTTGA (SEQ
 ID NO: 2)

AOLFR2 sequences:

15 MMMVLRNLSMEPTFALLGFTDYPKLQIPLFLVFLLMYVITVVGNLGMIIIIKINPKFHTPMYFFL
 SHLSFVDFCYSSIVTPKLEENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC
 NPLLYTVAMSQRLLCALLVAGSYLWGMFGPLVLLCYALRLNFSGPVNVINHHFCEYALISVSGS
 DILIPHLLLSFATFNEMCTLLIILTSYVFIVTVLKIRSVSGRHKAFSTWASHLTAITIFHGILFL
 YCVPSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:
 20 3)

ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCCACCTTTGCCCTTTTAGGTTTCACAG
 ATTACCCAAAGCTTCAGATTCCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAACCCCAAATTCACACTCCTATGT
 25 ACTTTTTCTTAGTCACCTCTCTTTGTTGATTTTGTGTTACTCTTCCATTGTCACTCCCAAGC
 TGCTTGAGAACTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA
 CTTCCTGTCCTGCACTGCTGTGGTGACAGAGTCTTCTTGTGCTGGCAGTGATGGCCTATGAC
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTACAGAGGCTCTGTG
 CCCTGCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCCTTGGTACTCCTTTGTTAT
 30 GCTCTCCGGTTAACTTCTCTGGACCTAATGTAATCAACCACTTCTTTTGTGAGTATACTGC
 TCTCATCTCTGTGTCTGGCTCTGATATACATCATCCCCACCTGCTGCTTTTTCAGCTTCGCCA
 CCTTCAATGAGATGTGTACACTGATCATCTCATCTTCTTCTATGTTTTTCACTTTTGTGACT
 GTACTAAAAATCCGTTCTGTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCTCCACC
 TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACCTCCAAA
 35 AACTCTCGGCAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA
 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTTCTGGAAGTTAATACA
 TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

AOLFR3 sequences:

40 MLLTDRNTSGTTFLLGFSDYPELQVPLFLVFLAIYNTVLGNIGLIVIIKINPKLHTPMYFFLSQ
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFFCTFVVTESFLLAVMAYDRFVAICNPL
 LYTVDMQSKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHHFCEFSLLSLSCSDTYI
 NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGILFLYCV
 PNSKNSRHTVKVASVFYTVVIPMLNPPIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

45 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTTACCCTCTTGGGCTTCTCAGATT
 ACCCAGAAGTCAAGTCCCACTCTTCTGTTTCTTCTGGCCATCTACAATGTCACTGTGCTA
 GGGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT
 TTTTCTCAGCCAACTCTCCTTTGTGGATTTCTGCTATTCTCCTCCATCATTGCTCCCAAGATG
 50 TTGGTGAACCTTGTGTCAAAGACAGAACCATTTCATTTTATAGCTGTGATGGCCTATGACCGC
 TTCGTGGCCATTTGCAACCCTCTGCTCTACACAGTTGACATGTCCAGAACTCTGCGTGC
 TGCTGGTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTCTGC
 TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC
 55 TACTCTCCCTTTCTTGTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC
 TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT

CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCCACCTG
ACTGCCATCACCATCTTCCATGGCACCATCCTCTTCCTTTACTGTGTGCCCAACTCCAAAAA
CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCCATGTTGAAT
5 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC
ACCAAAGTCTTCTCTTACTGA (SEQ ID NO: 6)

AOLFR4 sequences:

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTIITSQSLRSPMYFFLTFLS
LLDVMFSSVVAPKVIVDTLSKSTISLKGCLTQLFVEHFFGGVGIILLTVMAYDRYVAICKPLHY
10 TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFICDLFQLLTLACTDTHILGL
LVTNLNGMMCVAI FLILIASYTVILCSLKSYSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV
VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC
15 TGTGGAAAATATTTTCTGCTGTGTTTCTTGTCATGTATGTAGCCACAGTGCTGGAAAATCT
ACTTATTGTGGTAACTATTATCAAAAGTCAGAGTCTGAGGTACCTATGTATTTTTTTCTTA
CCTTCTTGTCCTTTTGGATGTGATGTTCTCATCTGTCGTTGCCCCCAAGGTGATTGTAGAC
ACCCTCTCAAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC
ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC
20 CATCTGTAAGCCCCTGCATACACGATCATGATGAGTCCACGGGTGTGCTGCCTAATGGTA
GGAGGGGCTTGGGTGGGGGATTTATGCACGCAATGATACAACTTCTCTTCATGTATCAAA
TACCCTTCTGTGGTCTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA
CTTGCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT
GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCCTGAAGTCT
25 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCACCTCACGGTGGTTG
TATTGTTCTTTGTCCCCTGTATTTTCTGTACATGAGGCCTGTGGTCACTACCCCATAGAC
AAGGCAATGGCTGTGTCAGACTCAATCATCACCCCATGTTAAATCCCTTGATCTATACAC
TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG
CTGGGAAATAA (SEQ ID NO: 8)

30

AOLFR5 sequences:

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTL LANLGMIALIQVSSRLHTPMYFFLSH
LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL
LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN
35 ETLLFLVATL NESVTIMILTSYLLILTILKMGS AGRHKAFTCASHLTAITVFHGTVLSIYCRP
SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKELRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACCTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC
CTGAGTTGAGAGTCTGCCTCTTCCTGCTGTTCCTTCTCATCTATGGAGTCACGTTGTTAGCC
40 AACCTGGGCATGATTGCACTGATTGAGGTGAGTCTCGGCTCCACACCCCATGTACTTTT
TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG
GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCCTAGGGTGCATGGTGCAATTCTACT
TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT
GTGGCCATCTGTAACCCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC
45 TGGCTTCTTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTGTGCTTAGCTCTT
AGGATCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT
AAGTCTTGTTGCTCTGATATCACTGTGAATGAGACACTGCTGTTCTGCTGGTGGCCACTTTG
AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT
GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCCACCTCACA
50 GCTATCACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCCAGTTCAGGCAATA
GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACTC
TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC
CAAAATTCACCTCCTAG (SEQ ID NO: 10)

AOLFR6 sequences:

MMASERNQSSTPTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMYFFLS
HLSLTDFCFSTVVPKLEENLVVEYRTISFSGCIMQFCFACIFGVTFETFMLAAMAYDRFVAVCK
5 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLDLDFCESTFINNFICDHSVIVSASYSDPYIS
QRLCFIIAIFNEVSSLIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCVPNP
KTSSLIVTVASVFYTVAIPLMLNPLIYSLRNKDINNMFELKLVVTKLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTCAG
AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTCGTCTACACAGTCACTGTA
10 GTGGGGAACCTGGGCATGATAATAATCATCAGACTCAATCAAACCTCCATACAATCATGT
ACTTTTTCTTAGTCACTTGTCTTGACAGACTTCTGTTTTTCCACTGTAGTTACACCTAAA
CTGTTGGAGAACCTGGTTGTGGAATACAGAACCATCTCTTTCTCTGGTTGCATCATGCAAT
TTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC
CGTTTTGTGGCAGTTTGTAAACCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC
15 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT
CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT
AATTGTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATTGCCA
TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC
ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAAACCTTCTCCACCTGTGCCTCCCACC
20 TGACAGCCATCACTATCTTCCATGGAACATCCTTTTCTTTACTGTGTTCTAATCCTAAA
ACTTCTAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGGCGATTCCAATGCTGA
ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT
CACCAAATTGATTACCCTGA (SEQ ID NO: 12)

AOLFR7 sequences:

MSYFYRLKLMKEAVLVKLPFTSLPLLLQTLRKSRLDMEIKNYSSSTSGFILLGLSSNPQLQKPLF
AIFLIMYLLAAVGNVLIIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLNVNLFSETKVISY
VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL
FRVLLMSRSLSCASHIHKHFFCDTQPVKLKSCSDTSSSQMVVMTETLAVIVTPFLCIIFSILRIMV
30 TVLRIPSAAGKWKAFSTCGSHLTAVALFYGSHIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN
PFIYSLRNKMDMKRGLKKLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTA
CATCTCTCCCACTGCTTCTCAAACCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA
35 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCAAACCTCAGCTGCAG
AAACCTCTCTTTGCCATCTTCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT
CATCCCGGCCATCTACTCTGACCCCAAGGCTCCACACCCCTATGTACTTTTTTCTCAGCACT
TGTCTTTTATGGATATCTGCTTACAAACAGTCATAGTGCCTAAGATGCTGGTGAATTTCTA
TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT
40 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG
CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT
TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT
CTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT
GCTCTGACACATCCTCCAGCCAGATGGTGGTGTGACTGAGACCTTAGCTGTCTATTGTGAC
45 CCCCTTCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT
CTGCAGCCGGGAAGTGGAAGGCCTTCTCTACCTGTGGCTCCACCTCACTGCAGTAGCCCT
TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTAAGTCACTGAGTGGTATGGG
ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG
CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAATTTACCGGTA
50 A (SEQ ID NO: 14)

AOLFR8 sequences:

MATSNHSSGAEFILAGLTQRPELQLPLFLFLGIYVTVVGNLGMIFLIALSSQLYPPVYYFLSH
LSFIDLCYSSVITPKMLNVNFVEENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY
55 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTLAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMYFKPPSS
TTMEKEKVSSVFYITIIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCATTCCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC
CAGAACTTCAACTGCCACTCTTCCTCCTGTTCCCTTGGAAATATATGTGGTCACAGTGGTGGG
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTACCCTCCAGTGTATTATT
TTCTCAGTCATTTGTCTTTTCATTGATCTCTGCTACTCCTCTGTGCATTACCCCTAAGATGCTG
GTGAACTTTGTTCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT
CTTCCTTATTTTTGTAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT
10 GTTGCTATCTGTGCGCCCACTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA
GTGTTGTCATTCTGTAGGTCTCATAACGGTCAGTCATTATTTTTGTGATATTCTCCCCTTATT
GACTCTGTCTTGTCTCCAGCACCCACATCAATGAGATTCTGCTGTTTATTATTGGAGGAGTT
AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTCATTTTCTCTAGTATCCT
15 TGGTATTCATTCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGAGCTCCCATCTCTTG
GCTGTGGGCATCTTTTTTGGGTCTATAACATTATGATTTTCAAGCCCCCTTCCAGCACTAC
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

AOLFR9 sequences:

MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFGNLNSHLHTPMYYFLFN
LSFIDL CYSSVFTPKMLMNFVSKKNIISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANIINHLYCDILPLLQLSCTSTYV
25 NEVVVLIVVGTNITVPSCITILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY
SSGSMEQGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

30 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCTGGCAACCCTTCTTTTTCTGTTCCTAGTGATCTACATTGTCAACCATGGTAGGC
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCCAAAATGCTAAT
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT
GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA
35 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCCACACCGGGTGCATGTTTAC
ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTTC
AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA
TATCACGGTACCCAGTTGTACCATCCTCATTCTTATGTTTTTCAATTGTCACTAGCATTCTTC
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGC
40 TCTGTCTCTGTTTTTTGGGTGAGCGGCATTATGTATATTAATAATTCTTCTGGATCTATGG
AGCAGGGAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCTCATC
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAATTCAG
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFNL
SFIDLCYSSVFTPKMLMNFVSKKNIISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLTLFCSANIINHLYCDILPLLQLSCTSTYVN
EVVVVLIVVGINIMVPSCITILISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS
50 SGSMEQGVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

55 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC
CAGAGTTCCGGCAACCCTTCTTTTTCTGTTCCTAGTGATCTACATTGTCAACCATGGTAGGC
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCCAAAATGCTAAT
GAACTTTGTATCAAAAAAGAATATTATCTCCTATGTTGGGTGCATGACTCAGCTGTTTTTCT

TTCTCTTTTTTGTCACTCTCTGAATGCTACATATTGACCTCAATGGCATATGATCGCTATGTG
 GCCATCTGTAATCCATTGCTGTATAAGGTACCATTGTCCCATCAGGTCTGTTCTATGCTCAC
 TTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGCTTAGA
 CTCACCTTCTGCAGTGCTAATATCATCAACCATTACTTGTGTGACATACTCCCCCTCCTCCA
 5 GCTTTCTGCAACGACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTATTAAT
 ATCATGGTACCCAGTTGTACCATCCTCATTTCTTATGTTTTTCATTGTCACTAGCATTCTTCA
 TATCAAAATCCACTCAAGGAAGATCAAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGCT
 CTGTCTCTGTTTTTTGGGTCAGCGGCATTTCATGTATATTAAATATTCTTCTGGATCTATGGA
 GCAGGGAAAAAGTTTCTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCTCTCATCT
 10 ACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAGA
 GAAGAAATATATTCTAA (SEQ ID NO: 20)

AOLFR11 sequences:

MTLRNSSSSVTEFILVGLSEQPELQLPLFLLFLGIYVFTVVGNLGLITLIGINPSLHTPMYFFLFNLS
 15 FIDLCYSCVFTPKMLNDFVSESIISYVGCMTQLFFCFVNSECYVLVSMA YDRYVAICNPLLY
 MVTMSPRVCFLLMFGSYVVG FAGAMAHTGSMRLRTFCDSNVIDHYLCDVLP LLQLSCTSTHV
 SELVFFIVVGVITMLSSISIVISYALILSNILCIPSAEGRSKAFSTWGSIIIAVALFFGSGTFTYLTTS
 FPGSMNHGRFASVFYTNVVPMLNPSIYSLRNKDDKLALGKTLKRVLF (SEQ ID NO: 21)
 20 ATGACTCTGAGAAACAGCTCCTCAGTGACTGAGTTTATCCTTGTGGGATTATCAGAACAGC
 CAGAGCTCCAGCTCCCTCTTTTCTTCTATTCTTAGGGATCTATGTGTTCACTGTGGTGGGC
 AACTTGGGCTTGATCACCTTAATTGGGATAAATCCTAGCCTTCACACCCCATGTACTTTTT
 CCTCTTCAACTTGTCTTTATAGATCTCTGTTATTCCTGTGTGTTTACCCCCAAAATGCTGA
 ATGACTTTGTTTCAGAAAGTATCATCTCTTATGTGGGATGTATGACTCAGCTATTTTTCTTC
 25 TGTCTTCTTGTCAATTCTGAGTGCTATGTGTTGGTATCAATGGCCTATGATCGCTATGTGGC
 CATCTGCAACCCCTGCTCTACATGGTCACCATGTCCCAAGGGTCTGCTTTCTGCTGATGT
 TTGGTTCTATGTGGTAGGGTTTGCTGGGGCCATGGCCCACTGGAAGCATGCTGCGACT
 GACCTTCTGTGATTCCAACGTCATTGACCATTATCTGTGTGACGTTCTCCCCCTCTTGCAGC
 TCTCCTGCACCAGCACCCATGTGAGTGAGCTGGTATTTTTTCATTGTTGTTGGAGTAATCACC
 30 ATGCTATCCAGCATAAGCATCGTCATCTCTTACGCTTTGATACTCTCCAACATCCTCTGTAT
 TCCTTCTGCAGAGGGCAGATCCAAAGCCTTTAGCACATGGGGCTCCCAACATAATGCTGTT
 GCTCTGTTTTTTGGGTGAGGACATTCACCTACTTAACAACATCTTTTCTGCTCTATGAA
 CCATGGCAGTTTGGCTCAGTCTTTTACACCAATGTGGTTCCCATGCTTAACCCTTCGATCT
 ACAGTTTGAGGAATAAGGATGATAAACTTGCCCTGGGCAAAACCCTGAAGAGAGTGCTCT
 35 TCTAA (SEQ ID NO: 22)

AOLFR12 sequences:

MERNHNPDN CNVLNFFFADKKNKRRNFGQIVSDVGRICYSVLSLGEPTTMGRNNLTRPSEFIL
 LGLSSRPEDQKPLFAVFLPIYLITVIGNLLIILAIRSDTRLQTPMYFFLSILSFVDICYVTVIIPKMLV
 40 NFLSETKTISYGECLTQMYFFLAFGNTDSYLLAAMAIDRYVAICNPFHYITIMSHRCCVLLLVLS
 FCIPHFHSLHLLTNQLIFCASNVIHHFFCDDQPVLKLSCSSHFVKEITVMTEGLAVIMTPFSCIII
 SYLRILITVLKIPSAAGKRKAFSTCGSHLTVVTLFYGSISYVYFQPLSNYTVKDQIATIIYTVLTP
 MLNPFYISLRNKDMKQGLAKLMHRMKCQ (SEQ ID NO: 23)
 45 ATGGAAAGAAACCACAATCCAGATAATTGTAATGTTTTAAATTTTTTCTTTGCTGATAAGA
 AGAATAAAAAGGAGAAATTTTGACAGATTGTATCAGATGTTGGAAGAATCTGTTACAGTG
 TTAGTTTATCTTTAGGTGAACCCACAACCTATGGGAAGAAATAACCTAACAAGACCCTCTGA
 ATTCATCCTCCTTGGACTCTCCTCTCGACCTGAGGATCAGAAGCCGCTCTTTGCTGTGTTC
 TCCCCATCTACCTTATCACAGTGATAGGAAACCTGCTTATCATCCTGGCCATCCGCTCAGA
 50 CACTCGTCTCCAGACGCCCATGTACTTCTTTCTAAGCATCCTGTCTTTTGTTGACATTTGCT
 ATGTGACAGTCATTATCCCTAAGATGCTGGTGAACCTTCTTATCAGAGACAAAGACCATCTC
 TTACGGTGAGTGTCTGACCCAGATGTACTTTTTCTTAGCCTTTGGAACACAGACAGTTAC
 CTGCTAGCAGCCATGGCCATTGACCGCTATGTGGCCATATGTAATCCCTTCCACTACATCA
 CCATTATGAGTCACAGATGCTGTGTCCTGCTTCTGGTTCTCTCCTTCTGCATTCCACATTTT
 55 CACTCCCTCCTGCACATTCTTCTGACTAATCAGCTCATCTTCTGTGCCTCCAATGTCATCCA
 TCACTTTTTCTGCGATGATCAACCAGTGCTAAAATTGTCTGTTCTCTCCATTTTGTCAAAG

AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCTTCAGCTGCTGGAAAGCGTAAA
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA
TGTCTATTTTCAGCCCCCTGTCCAATACTGTCAAGGATCAAATAGCAACAATTATCTAC
5 ACCGTACTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

AOLFR13 sequences:

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTIHVLSHLDPHLHNP MYFFFSNL
10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLSTECVLLGVMAFDRYAAVCRPL
HYTVVMHPCLYVLMASWSVIGFANSLLQTVLILLTLCGRNKLHFLCEVPPLKLACVDYT
MNESELFVSVIILLVPVALIIFSYSQIVRAVVRKISATGQRKVFGTCGSHLTVVSLFYGTAIYAY
LQPGNNYSQDQGXISLFYTIITPMINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:
25)

15 ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTTGATCTTCTATATCTTCACTTTGCTGGGG
AACAAAACCATCATTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTTT
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG
20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCAGCTGTACAT
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT
GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA
TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCCCTCCATTGCT
25 CAAGCTTGCCTGTGTTGACACTACTATGAATGAATCTGAACCTCTTCTTTGTGAGTGTCATTA
TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTGAGGGCAGTCGTG
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTTTGGGACATGTGGCTCCACCTCACA
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAACACTCTC
30 TCAGGATCAGGGCAAGKTCATCTCTCTTCTACACCATCATTACACCCATGATCAACCCC
CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG
AACTACGACTCCAGATGA (SEQ ID NO: 26)

AOLFR14 sequences:

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL
35 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYSIAIGPKMLVDLLLPRATIPYTACALQMF
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGAVSAFVHTTLTF
RLSFCRSRKINSFFCDIPLLAISCDTSLNELLFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRNKE
VKEALRQTWRSRHFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG
GATGAACTCAGAGAACCTCACCCGGGCGCGGTTGCCCTGCTGAATTCGTCCTCCTGGGC
ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCCTGACCTGCCTGCCTGTCTACCTGG
TGAGCCTGCTGGGAAACATGGGCATGGCGCTGCTGATCCGCATGGATGCCCGGCTCCACA
45 CACCTATGTACTTCTTCTGGCCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCGAGCCACCATCCCTTACACAGCCTGTG
CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTTGCTTGCTGGCAGCCAT
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTGCGAG
CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCTTTGTTC
50 ACACAACCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG
CGATATCCCTCCACTGCTGGCCATCTCGTGCAGTGACACCAGTCTCAATGAACTCCTTCTCT
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTTAGCTATCACGGTGCTTATGGCTT
CATCGCTGGGGCTGTGATCCACATGCGCTCGGTGAGGGCAGTCGGCGAGCAGCCTCCAC
CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTCATGTACCTG
55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

AOLFR15 sequences:

5 MRENNQSSTLEFILLGVTGQQEQEDFFYILFLFIYPITLIGNLLIVLAICSDVRLHNP MYFLLANLS
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYILAAMAYDRAVAISHPLH
YTTIMSPRSCIWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLLKLSCDIHFHV
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFQVPSTKGV LKAFSTCGSHLT VVS LYYGTVMGTYFR
PLTNYSLKDAVITVMYTA VTPMLNPFYISLRNRDMKAALRKL FNKRIS (SEQ ID NO: 29)

10 ATGAGGGAAAATAACCAAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC
AGGAACAGGAAGATTTCTTCTACATCCTCTTCTGTTCAATTTACCCCATCACATTGATTGGA
AACCTGCTCATTGTCCTAGCCATTTGCTCTGATGTTGCGCTT CACAACCCCATGTATTTCT
CCTTGCCAACCTCTCCTTGTTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG
15 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT
CATGATAGCCTTGGGTAACACAGACAGCTATATTTTGGCTGCAATGGCATATGATCGAGCT
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC
TAGTCTGTCCTTCTGTGGCAACCAGGAAGTGCCAACTTCTACTGTGACATTACCCCTTG
20 CTGAAGTTATCCTGTTCTGACATCCACTTTTCATGTGAAGATGATGTACCTAGGGGTTGGCA
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC
AGGTTCTTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCCCACCTCACGGT
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTTGACCAATTATAGCC
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTTCAT
25 CTACAGTCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT
CTCCTCGTAA (SEQ ID NO: 30)

AOLFR16 sequences:

30 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAVAGNLGMIVLIQANAWLHMPMYFFLSH
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVQCYLFIALVHVEIYILAVMAFD RYMAICNP LL
YGSRMKS SVCSFLITVPYVYGALTGLMETMWTYNLAFCGPNEINH FYCADPPLIKLACSDTYN
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR
PPSKESVEQGKMVA VFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG
GAATTACAAATTCCTCTTACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA
ACCTTGGCATGATTGTCCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTC
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG
AGATTTTCTTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGCAGTGTTACCTT
40 TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC
ATCACGGTGCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA
ACCTAGCCTTCTGTGGCCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT
TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG
45 AACCTTCTTTTCTCTCTTCATCATATGTATTTCTACCTTTACATTTTCCCTGCTATTTTA
AAGATTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTCTACCTGTGGCTCCCATCTGACAG
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

AOLFR17 sequences:

MLNFTDVT EFILLGLTSRREWQVLFFIIFLVVYIITMVG NIGMMVLIKVSPQLNNP MYFFLSHLS
FVDVWFSSNVTPKMLENLFSDDKKTITYAGCLVQCFFFIALVHVEIFILAAMAFDRYMAIGNPLL
55 YGSKMSRVVCIRLITFPYIYGFLTSLAATLWYGLYFCGKIEINH FYCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIIISYLFILAILMRSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT
GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC
GGCATGATGGTGTTAATCAAGGTCAAGTCCCTCAGCTTAACAACCCCATGTACTTTTTCTCA
GTCACCTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC
CTGTTTTTCAGATAAAAAACAATTACTTATGCTGGTGTGTTAGTACAGTGTTCCTTCTTCAT
TGCTCTTGTCCATGTGGAAATTTTTATTCTTGTCTGCGATGGCCTTTGATAGATACATGGCAA
10 TTGGGAATCCCTCTGCTTTATGGCAGTAAAATGTCAAGGGTTGTCTGTATTGACTGATTAC
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT
ACTTCTGTGGAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGATCATACTTGCCGGCATTAACCTC
ACATATCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATTATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 34)

20

AOLFR18 sequences:

MSNTNGSAITEFILLGLTDCPELQSLFVLFLVYLVTLGNLGMIMLMRLDSRLHTPMYFFLT
NLA FVDLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP
LRYSVKTSRRVCICLATFPYVYGFS DGLFQAILTFRLTFCRSNVINHFYCADPPLIKLSCSDTYVK
25 EHAMFISAGFNLSSSLTIVLVSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLFCMYI
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKQALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC
CGGAACTCCAGTCTCTGCTTTTTGTGCTGTTTCTGGTTGTTTACCTCGTCACCCTGCTAGGC
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTACACGCCCATGTACTTCT
TCCTCACTAACTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC
GACTAATATCGTATCTGAGAAGACCATTTCCTTTGCTGGTTGCTTTACACAGTGCTACATTT
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT
GGCCATATATGACCCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG
35 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCTGACCTCCG
CCTGACCTTCTGTAGATCCAATGTCATCAACCATTCTACTGTGCTGACCCGCCGCTCATT
AGCTTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTCATATCTGCTGGCTTCAAC
CTCTCCAGCTCCCTACCATCGTCTTGGTGTCTATGCCTTCATTCTTGTGCTGCCATCCTCCG
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC
40 TGTCACCCTGTTTTATGGGACTCTCTTTGCATGTATATAAGACCACCAACAGATAAGACT
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTTGAAGAATGTCCTGAGATGA
(SEQ ID NO: 36)

45 **AOLFR19 sequences:**

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLIILAIYSDPRLHTPMYFFLSNL
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAIDRLVAICNPLH
YDVVMKPWHCLLMLLGSCSISHLHSLFRVLLMSRSLFCASHIHKHFFCDTQPVLKLSGSDTSSSQ
MVVMTETLAVIVTPFLCTIFS YLQIIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFYGSVIYVYFR
50 PLSMYSVMKGRVATVMYTVVTPMLNPFYIYSLRNKDMKRGLKKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT
55 TTTTCTCAGCAACTTGCTTTTCATGGATATCTGCTTCAACAGTCATAGTGCTTAAGATG
CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT

ACTTCTTCATGGCATTGTTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA
 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTAT
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAAGCACTTTTCTGTGACACCCAGCCTG
 5 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT
 AGCTGTCATTGTGACCCCTTCTGTGTACCATCTTCTCCTACCTGCAATCATCGTCACTG
 TGCTCAGAATCCCTCTGCAGCCGGAAGTGAAGGCCTTCTCTACCTGTGGCTCCACCT
 CACTGTAGTGGTCTGTCTATGGGAGTGTCTATGTCTATTTTAGGCCTCTGTCCATGT
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA
 10 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTGAAGAAATTAAGAC
 ACAGAATTTACTCATAG (SEQ ID NO: 38)

AOLFR20 sequences:

MVEENHTMKNEFILTGTDFHPELKTLLFVFFAIYLYLITVVGNI SLVALIFTHCRLHTPMYIFLGN
 15 LALVDSCCAITPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPLYRLSCVDPF
 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP
 NLLEEGGNDIPAILFTIVVPLLNPFIYSLRNKEVISVLRKILLIKISQGSVNK (SEQ ID NO: 39)
 20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTTACAGATCACC
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCGTGGTGGG
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTACACACCAATGTACATC
 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGCTGTGCCTGTGCTATTACCCCCAAAATGTT
 AGAGAACTTCTTTCTGAGGGCAAAGGATTTCCCTCTATGAATGTGCAGTACAGTTTAT
 25 TTTCTTTGCACTGTGGAACTGCAGACTGCTTCTTCTGGCAGCAGTGGCCTATGACCGCT
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAACTCTGCATTCA
 GATGACCACAGGCGCCTTCATAGCTGGAATCTGCATTCCATGATTATGTAGGGCTTGTA
 TTTAGGTTAGTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT
 GTATAGACTCTCCTGTGTTGACCCCTTTCATCAATGAAGTGGTCTTATTCATCTTCTCAGGTT
 30 CAGTTCAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATCTTCTTACTATT
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTTCTACTGTGCATCCCACTTTT
 CATCAGTTTCAATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA
 GAAGGAGGTAATGATATACCAGCTGCTATTTTATTACAATAGTAGTTCCCTTACTAAATC
 CTTTCATTTATAGTCTGAGAAACAAGGAAGTAATAAGTGTCTTAAGAAAAATTCTGCTGAA
 35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

AOLFR21 sequences:

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVVTVTVSETLGSPMSFFLAGL
 TFIDIIYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMA YDRYVAICKPLHYLV
 40 IMRQWVCVLLLVVSWVGGFLQSVFQLSIYGLPFCGPNVIDHFFCDMYPLLKLACTDTHVIGLL
 VVANGGLSCTIAFLLLISYGVILHSLKKLSQKRAHSTCSSHITVVVFFVPCIFMCARPAR
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)
 45 ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCCTCTTGGGCTTACACAGAATCCAAAG
 GAGCAGAAAGTACTTTTGTATGTTCTTGCTCTTCTACATTTTGACCATGGTGGGCAACCT
 GCTCATTGTAGTGACCGTAAGTGTGAGTGTGAGACCTGGGCTACCAATGTCCTTCTTTCTT
 GCTGGCTTAACATTTATAGATATCATTTATTCTTTCATCCATTTCCCCCAGATTGATTTTCA
 CTTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCAGCTCTTTATCGAGC
 50 ACCTTTTGGTGGGTCAGAGGTCTTCTCCTGTTGGTGATGGCCTATGACCGCTATGTGGC
 CATCTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAATGGGTGTGTGTTTGTGCTG
 GTAGTGTCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC
 TCCCATCTGTGGCCCCAATGTCATTGATCATTTTTTCTGTGACATGTATCCCTTATTGAAA
 CTGGCCTGCACTGACACCCATGTTATTGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT
 GCACTATTGCGTTTCTGCTCTTACTCATCTCTTATGGTGTGATCCTGCACTCTCTAAAGAAA
 55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCCACATCACTGTGGTTG
 TCTTCTTCTTGTTCCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

AOLFR22 sequences:

5 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLITYXXTVVGNLLIVVDIIASPLGSPMYFFLAC
LSFIDAAYSTTISPKLIVGLFCDKKTISFQGCMGQLFIDHFFGGAEVFLLVVMACDRYVAICKPL
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI
GLTVVVNSGAICMVIFNLLISYGVLSSSLKTYSQEKRGKALSTCSSGSTVVVLFVPCIFIYVRP
10 VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIIGGVSVLM (SEQ ID NO:
43)

ATGAGACANNNNNAACAATATNACAGAATTTGTCTCCTGGGCTTTTCTCAGGATCCTGGTG
TGNNNAAAGCATTATTTGTTCATGTTTTACTCACATACNNNNNNACAGTGGTGGGGAACCT
GCTCATTGTNGTGGATATTATTGCCAGCCCTTNNNTGGGTTCCCAATGTATTTCTTCCTTG
15 CCTGCCTGTCAATTTATAGATGCTGCATATCCACTACCATTCTCCCAAGTTAATTGTAGGC
TTATTCTGTGATAAAAAGACTATTTCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC
ATTTCTTTGGTGGGGCTGAGGTCTTCTCTGGTGGTGCATGGCCTGTGATCGCTATGTGGC
CATCTGTAAGCCACTGCACATTTTGACCATCATGAATCGACAGGTTTGCTTCCTTCTGTTGG
TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTCAAATTGTTGTGTACAGTCTCCCT
20 TTCTGTGGTCCCNATGTCAATTGTTCAATTCAGTTGTGACATGCACCCATTACTGGAAGTGGC
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGGAGCAATCTGTATG
GTCATTTTCAACCTTCTGTTAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAACTTACAG
TCAGGAAAAGAGGGGTAAAGCCTTGCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCTC
TTTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAACCTTCTACTGATAAGTT
25 CATGACTGTGTTTTATACCATTATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA
AATTCAGAGATGAGAAAATGCTATAGAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

AOLFR23 sequences:

30 MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS
HLSLLDACYSVTIPQILATLATGKTVISYGHCAAQFFLTICAGTECFLLAVMAYDRYAAIRNP
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTTCTFTLSFCKDNQINFFFCDLPLLLKLACSDTA
NIEIUIFFGNFVILANASVILISYLLIKTILVKSSGGRKTFSTCASHITAVALLFFGALIFMYLQS
GSGKSLEEDKVVSIFYTVVIPMLNPLIYSLRNKDVKDFAFRKVARRLQVSLSM (SEQ ID NO: 45)

35 ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC
CCAAATTGGAGATTCCCCTCTTTCTGGTGTCTCTGAGTTTCTACCTAGTCACCCTTCTTGGG
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTCTACACCCCAATGTACTTCT
40 TCCTGAGCCACCTCTCCCTGCTGGATGCCTGTTACACCTCAGTCATCACCCCTCAGATCCTA
GCCACATTGGCCACAGGCAAAACGGTCATCTCCTACGGCCACTGTGCTGCCAGTTCTTTT
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCCATCCTGCGTACCACTTGACCT
45 TCACCCTCTCCTTCTGTAAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG
CTGAAGCTTGCCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT
TTGTGATTTTGGCCAATGCCTCCGTCATCCTGATTTCTCTATCTGCTCATCATCAAGACCAT
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA
CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA
50 TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC
CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

AOLFR25 sequences:

55 METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITVMGNILIIITVTSDSLHTPMYFLLRN
LAVLDLCFSSVTAPKMLVDLLSEKKTISYQGCMGQIFFFHFLGGAMVFFLSVMAFDRLIAISRPL
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVLRRLACTDT

SLLEFLKISNSGLLDVWFFLLMSYLFILVMLRSHPGEARRKAASCTCTTHIIVVSMIFVPSIYLY
ARFPTPFMDKLV SIGHTVMTPMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

5 ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCTCTGGGGCTCTCGCAGACTC
GGGAGCTCCAGCGTTTCTGTTTCTAATGTTCTGTTTGTCTACATCACCCTGTTATGGGA
AACATCCTTATCATCATCACAGTGACCTCTGATTCCCAGCTCCACACACCCATGTACTTTCT
GCTCCGAAACCTGGCTGTCCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAATGCTAG
TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT
CTTCCACTTTTTTGGGAGGTGCCATGGTCTTCTTCTCTCAGTGATGGCCTTTGACCGCCTCA
10 TTGCCATCTCCCGGCCCTCCGCTATGTCACCGTCATGAACACTCAGCTCTGGGTGGGGCT
GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC
CCACTGCCCTTCTGTGGCCCCAACATTTTGGATAACTTCTACTGTGATGTTCCCCAAGTACT
GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG
CTGGATGTCGCTCTGGTTCTTCTCCTCCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG
15 GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCACCCACATCATCGT
GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCCGCCCTTCACTCCATTCCCTA
TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA
TACCCTGAGGAACCAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT
TTGA (SEQ ID NO: 48)

20

AOLFR26 sequences:

MAAKNSSVTEFILEGLTHQPGLRIPLFFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNL
LIDFCSTTTITPKMLMSFVSRKNISFTGCMTQLFFFCFFVVSSEFILSAMAYDRYVAICNPLLYT
VTMSCQVCLLLLGA YGMGFA GAMAHTGSIMNLTFCADNLVNHFMCDILP LLELSCNSSYMN
25 ELVVFIVVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP
LSILPLEQGVSSLFYTHVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG
GACTGCGGATCCCCCTCTTCTTCTGTTTCTGGGTTTCTACACGGTCACCGTGGTGGGGAA
30 CCTGGGCTTGATAACCTGATTGGGCTGAACCTCTCACCTGCACACTCCCATGTACTTCTTCC
TTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAATGCTGATG
AGTTTTGTCTCAAGGAAGAACATCATTTTCTTCCAGGGGTGTATGACTCAGCTCTTCTTCTT
CTGCTTCTTTGTCTCTCTGAGTCCTTCATCCTGTGACGATGGCGTATGACCGCTACGTGG
CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG
35 TTGGGTGCCTATGGGATGGGGTTTGCTGGGGCCATGGCCACACAGGAAGCATAATGAAC
CTGACCTTCTGTGCTGACAACCTTGTCATCATTTTCATGTGTGACATCCTTCTCTCCTTGA
GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTGGTGGCTGTTGAC
GTTGGAATGCCATTGTCACTGTCTTTATTCTTATGCCCTCATCCTCTCCAGCATTCTACA
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAAGTTCCACATAATTGTA
40 GTTTCTCTTTTCTTTGGTTCTGGTGCTTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC
GAGCAAGGGAAAGTGTCTCCTGTTCTATACCATAATAGTCCCCGTGTTAAACCCATTAA
TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA
TCTTTTCTTAA (SEQ ID NO: 50)

45 **AOLFR27 sequences:**

MPSQNYSISEFNLFGFSAFPQHLLPILFLYLLMFLFTLLGNLLIMATTWIEHRLHTPMYFLCTL
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR
YNVLMSPRDCAHLVACTWAGGSVMGMMVTTIVFHLTFCGSNVIIHFFCHVLSLLKLACENKT
SSVIMGVMLVCVTALIGCLFLIILSYVFIVAAILRIPSAEGRHKTFSTCVSHLTVVVTHYSFASFIY
50 LKPKGLHSMYSDALMATTYTVFTPLSPIIFSLRNKELKNAINKNFYRKFCPPSS (SEQ ID NO:
51)

ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC
CCAGCACCTCCTGCCCATCTTGTTCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG
55 GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT
CTTCTTGTCACCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC

AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC
TGTGGATCCCACCTCACCATGGTTGGTTTCTCTACGGCACCATCATTTGTGTCTACTTCCA
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT
ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACCTCT
5 GCAGGCTGCTTGAATGGGTGAAGGTAGACCCCTGA (SEQ ID NO: 56)

AOLFR30 sequences:

MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMIT
LICLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNIISYAGCMSQLYFFLVFVIAEC
10 YMLTVMAYDRYVXXCHPLLNIIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY
FCDILPLMKLSCSSTYDVENTVFFSAGFNIIVTS�TVLVSYFILSSILGISTTEGRSKAFSTCSSHL
AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAQVQKTLRGK
LF (SEQ ID NO: 57)

15 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG
GAAATCACTCTACAGTGACAGAGTTTCTCAAGGGTTTAACGAAGAGAGCAGACCTCC
AGCTCCCCCTCTTTCTCTCTCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC
ATGATCACTCTAATTTGTCTGAACCTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA
TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCATTACCCCTAAGATGCTGGTGAACCTTG
20 TGTGAGAGAAAAACATCATCTCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCTTGT
TTTTGTCAATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC
TGCCACCCTTTGCTTTACAACATCATTATGTCTCATCACACCTGCCTGCTGCTGGTGGCTGT
GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAACTGGCCTCATGTTAAACTGCC
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCCTG
25 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC
ACGAGCTTAACAGTTCTTGTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC
CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCCACCTTGACGCCGTGGGAAT
GTTCTATGGATCAACTGCATTCATGTACTTAAACCCTCCACAATCAGTTTCTTGACCCAG
GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCCTAATCTACA
30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT
GA (SEQ ID NO: 58)

AOLFR31 sequences:

MG TGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIIVLIRSHHLHTPMYIFLCHL
35 AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAECFLAAMAYDRYVAICSP
LLYSTCMSPGVCILVGM SYLGGCVNAWTFIGCLLRLSFCGPNKVNHFCDYSPLKLACSHDF
TFEIIPIASSGSIIIVATVCVIAISYIYLITILKMHSTKGRHKAFSTCTSHLTA VTLFYGTITFIYVMP
KSSYSTDQNKVVS VFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA
CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTACCTTAATGGGT
AATATCAGCATAATTGTATTGATCAGAAGAAGTCATCATCTTCATACACCCATGTACATTT
TCCTCTGCCATTTGGCCTTTGTAGACATTGGGTACTCCTCATCAGTCACACCTGTCATGCTC
45 ATGAGCTTCCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT
CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA
TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT
TAGTGGGCATGTCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT
AAGACTGTCCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTCACCACTTT
TGAAGCTTGCTTGTTCCCATGATTTTACTTTTGAAATAATTCCAGCTATCTCTTCTGGATCT
50 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCCTACATCTATATCCTCATCACCATCCT
GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCCACCTCACT
GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCCAAGTCCAGCTACTC
AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC
CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA
55 AAAATATTTTCTTGA (SEQ ID NO: 60)

AOLFR32 sequences:

MNSLKDGNHTALTGFILLGLTDDPILRVILFMIILSGNLSIIILIRISSQLHHPMYFFLSHLAFADM
AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAFFATVECVLLAAMAYDRFVAICSPLLYSTK
MSTQVSVQLLL VVYIAGFLIAVS YTTSFYFLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLSF
5 SSGSIIVVTVCVIAVCYIYLITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST
DQNKVVS VLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRSTSNNDIT (SEQ ID
NO: 61)

ATGAATTCCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA
10 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA
ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT
GGCTTTTGCTGACATGGCCTATTCATCTTCTGTACACACCAACATGCTTGTAACCTTCCTGG
TGGAGAGAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT
TGCAACAGTCGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC
15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG
TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCCTTCTATTTTTTACTCTTCT
GTGGACCAAATCAAGTCAATCATTTTTTCTGTGATTTGCTCCCTTACTTGAACCTCTCCTGT
TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTTCTTCTGGATCCATCATTGTGGTCAC
TGTGTGTGTCATAGCCGTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA
20 CTGAGGGGACCAACAAGGCCTTCTCCACCTGCACTTCCCACCTCACTGTGGTTACCCTGTT
CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCAGAAC
AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC
TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTTAGAAAAATACTTTCTC
ATGATGCTTGTTATTTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

AOLFR34 sequences:

MLEGVEHLLLLLLLLTDVNSKELQSGNQTSVSHFILVGLHHPQLGAPLFLAFLVIYLLTVSGNG
LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHFLGCT
ECFLYTL MAYDRFLAICKPLHYATIMTHRVCNSLALGTWLGGTIHSLFQTSFVFRLPFCGPNRV
30 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST
CAAHLT VVIVVYPCTFIYLRPCSQEPLDGVVAVFYTVITPLLNSIYTLCNKEMKAALQRLGG
HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG
35 AACTGCAAAGTGGAACCAAGACTTCTGTGTCTCACTTCATTTGGTGGGCCTGCACCAACC
ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTCTTGTCTATCTCCTCACTGTTTCTG
GAAATGGGCTCATCATCCTCACTGTCTTAGTGGACATCCGGCTCCATCGTCCCATGTGCTT
GTTCTGTGTACCTCTCCTTCTTGGACATGACCATTCTTGTGCTATTGTCCCCAAGATGC
TGGCTGGCTTTCTTGGGTAGTAGGATTATCTCCTTGGGGGCTGTGTAATCCAATATTT
40 TCTTTCCATTCTGGGCTGTACTGAGTGCTTCCCTTTACACACTCATGGCTTAGACCGTTT
CCTTGCCATTGTAAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC
TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTGTATT
CCGGCTGCCCTTCTGTGGCCCCAATCGGGTTCGACTACATCTTCTGTGACATTCTGCCATGC
TGCCTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACTTTGCAGACATTGGCTT
45 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCCTATGGCTATATTGTAGCTGCCATCC
TGCGAATTCGTCAGCAGATGGGCGCCGCAATGCCTTCTCCACTTGTGCTGCCACCTCAC
TGTTGTCAATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCTTGTTACAGGAGC
CCCTGGATGGGGTGGTAGCTGTCTTTTAACTGTCATCACTCCCTTGCTTAACTCCATCATC
TACAACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA
50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

AOLFR35 sequences:

MEPLNRTEVSEFFLKGFSGYPALEHLLFPLCSAMYLVTLLGNTAIMAVSVLDIHLHTPVYFFLG
NLSTLDICYTPTFVPLMLVHLLSSRKTSFAVCAIQMCLSLSTGSTECLLAITAYDRYLAICQPL
55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT
SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTIYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCTCCTGGG
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCGTGTACTTC
TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCCTCTGATGCT
GGTCCACCTCCTGTCTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC
10 TGAGCCTGTCCACGGGCTCCACGGAGTGCTGCTACTGGCCATCACGGCCTATGACCGCTA
CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGCTG
CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACTTCACCTGCAAGATCCTGGCAGT
GCTGAAGCTGGCATGCGGCAACACGTGCGTCAGCGAAGACTTCCTGCTGGCGGGCTCCAT
15 CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTGCTACTTGCTCATCCTGGCCACCA
TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG
GAAGCCACATCTCTGATGAGGTCTTCACAGTCCTCTATGCCATGGTCACGACCATGCTGA
ACCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG
20 GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

AOLFR36 sequences:

MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG
CLTQMSFLVLVFIACIVDMFLTVMAYDCFVAICRPLHYVIVNPHLCVFFVLVSFFLSLLDSQLHS
WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYDNTMFGFLPISGILLSYKIVPSILRIS
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFYIS
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTCAGCTCTGACTCCC
ACCCCCACACACCCATGTACTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
30 TTGGCCACGGTTCCTCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCTT
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTGCGCCCTCTGCACTACCCAGTCATC
GTGAATCCTCACCTCTGTGTCTTCTTCGTTTTGGTGCTCTTTTCTTACGCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTACCTTCTTCAAGAATGTGGAAATCTCTAATT
35 TTGCTGTGAGCCATCTCAACTTCTCAAGCTTGCTCTTATGACAGCGTCATCAATAGCATA
TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCATTTCAGGGATCCTTTTGTCTTAC
TATAAAATTGTCCCTCCATTCTAAGGATTCATCATCAGATGGGAAGTACAAAGCCTTCT
CAGCCTGTGGCTGTCACCTGGCAGTTGTTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT
40 GTGGTCACCCCATGCTGAACCCTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG
CCCTGTGGAGGGTGTGCAACAAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCTTAG
(SEQ ID NO: 68)

AOLFR37 sequences:

MEKANETSPVMGFVLLRLSAHPELEKTFVLLMYLVILLGNGVLILVTILDSRLHTPMYFFLG
NLSFLDICFTTSSVPLVLDSFLTQETISFSACAVQMAISFAMAGTECLLLSMMAFDRYVAICNP
LRYSVIMSKAAAMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS
INVISMEVTNVIFLGVPLFISFSYVFIITILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLFFMYG
50 KPKSKDSMGADKEDLSDKLIPLFYGVVTPMLNPIIYSLRNKDVKAARRLLRPKGFTQ (SEQ ID
NO: 69)

ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC
ACCCAGAGCTGGAAAAGACATTCTTCGTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT
55 GGGCAATGGGGTCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCATGTAC
TTCTTCTAGGGAACCTCTCCTTCTGGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

CCTGGACAGCTTTTTGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG
GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGTGATC
GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT
GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGTGCTTCCGTGGTACACACATCCTTG
5 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCATCAACCACTTCACCTGTGAGATTCTGG
CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA
TGTGATCTTCCTAGGAGTCCCGTTCTGTTTCATCTCTTTCTCCTATGTCTTCATCATCACCA
CCATCCTGAGGATCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCA
CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT
10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG
GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG
CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

AOLFR38 sequences:

15 MYLVTVLRNLLIILAVSSDHLHTPMCFFLSNLCWADIGFTSAMVPMIVDMQSHSRVISYAGC
LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW
IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFIYLDSIMFGFLPISGILLSYANNVPSILRISS
SDRKSKAFTSCGSHLAVVCLFYGTGIGVYLTSVSPPPRNGVVASVMYAVVTPMLNPFYISLR
NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

20 ATGTACCTGGTCACGGTGTGCTGAGGAACCTGCTCATCATCCTGGCTGTGCTGCTGACTCCC
ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC
TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG
CGGGCTGCCTGACACAGATGTCTTCTTTGTCTTTTGCATGTATAGAAGACATGCTCCTG
25 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTCACCCCCTGCACTACCCAGTCATCA
TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCCTCAGCCTGTTGGATTCC
CAGCTGCACAGTTGGATTGTGTTACAATTACCTTCTTCAAGAATGTGGAAATCTCCAATT
TTGTCTGTGACCCATCTCAACTTCTCAACCTTGCTGTTCTGACAGTGTCAATAGCATA
TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTACAGGGATCCTTTTGTCTTAC
30 GCTAACAAATGTCCCCTCCATTCTAAGAATTTTCATCATCAGATAGGAAGTCTAAAGCCTTCT
CCACCTGTGGCTCTCAGCTGGCAGTGTGTTGCTTATTTTATGGAACAGGCATTGGCGTGTA
CCTGACTTCAGCTGTGTGTCACCCACCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT
GTGGTCACCCCATGCTGAACCCTTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG
CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT
35 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

AOLFR39 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVCVISECYMLAAMACDRYVAICSP
40 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIKHIFYCDIVPLIKLSCSSTYDEL
LIFVIGGFNMVATSLTIIISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS
SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

ATGGGTGTAAAAAACCACTCCACAGTGACTGAGTTTCTTCTTTTTCAGGATTAACCTGAACAAG
45 CAGAGCTTCAGCTGCCCCCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG
AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTACTAT
TTCCTGAGTAGTTTGTCTTTTTTAGATTTCTGCTATTCTTCTGTCAATTACCCCTAAAATGCT
ATCAGGGTTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTCAGCTGTTTT
TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC
50 GTGGCCATCTGCAGCCCACTGCTCTACAGGGTCATCATGTCCCCTAGGGTCTGTTCTCTGC
TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT
CAGGTTGTCTTTCTGTGGATCAAACATCATTAAACATTATTTCTGTGACATTGTCCCTCTTA
TAAACTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTCAATTGGTGGATTT
AACATGGTGGCCACAAGCCTAACAAATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT
55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCCACCTGACA
GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC

ACTCACCCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSSTVTPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
RYTNMMTGRSCALLATGTWLSGSLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTS
ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVVLCFFGPGLFIYL
10 RPSRDALHGVVAVFYTTLTPLFNPVVYTLRNKEVKKALLKLKNGSVFAQGE (SEQ ID NO:
75)

ATGTCCAACGCCACCCTACTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCCTCTTTGGAATCTTCCTGGTGGTTACGTGCTCACTGTGCTGGGGAACCT
15 CCTCATCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA
CAAACCTGTCCTTCATTGACATGTGGTCTCCACTGTCACGGTGCCCCAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGTACCT
GGCCATCAGTTACCCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG
20 GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGCTGTCCTATGTGTCCATCGTCTGTTCCATCCT
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTACAGACCTGTGCCTCCCACTGTATC
25 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGGACGC
CTTGCATGGGGTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTCAACCCTGTTGTGT
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTAT
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSHLIQFLVFLGLMVYIVTATGKLLIIVLSWIDQRLHIQMYFFLRN
FSFLELLLVTVVVPKMLVVILTDHTISFVSCIIQSYLYFFLGTTDFLLAVMSLDRLAICRPLR
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLLRLSCGDTH
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAAERRKAFSTCASHLTVVVIIYGSSIFLY
35 IRMSEAQSKLLNKGASVLSCHIITPLNPFIFTLRNDKVQQALREALGWPRLTAVMKLRVTSQRK
(SEQ ID NO: 77)

ATGAACCCTGAAAACCTGGACTCAGGTAACAAGCTTTGTCCTTCTGGGTTTCCCCAGTAGCC
ACCTCATACAGTTCCTGGTGTTCCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC
TTCCTGCGGAATTTCTCCTTCTGGAGCTGTTGCTGGTAACTGTTGTGGTTCCCAAGATGCT
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCCTACC
TCTACTTCTTTCTAGGCACCACTGACTTCTTCTTGGCCGTCATGTCTCTGGATCGTTAC
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCTTTGCCCCACTGTCTCATGGCC
AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT
CAGGCTTTCTTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTCATGCTCTCTACGTTG
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTATGCCTGCATTCTTGCCACTGTTCT
CAGGGCCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTCCACTTGCGCCTCGCATCTTACA
50 GTGGTGGTCATCATCTATGGCAGTCCATCTTTCTCTACATTCTGATGTCAGAGGCTCAGTC
CAAACCTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCCTCTTGAACCA
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC
CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:
78)

55

AOLFR42 sequences:

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL
GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFHFIGGIKIFLLTVMAYDRYIAISQPL
HYTLIMNQTVCALLMAASWVGFIHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV
5 LELLMVSNNGLVTLMCFLVLLGSYALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCIYVY
TRPFRTPMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH
(SEQ ID NO: 79)

10 ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT
GGGAGCTTCGGTTTGTCTTCTCACTGTTTCTCTGCTGTGTATTTTATGACTGTAGTGGGA
AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTCT
CTTGGGCAATCTTTCTTCTGGACTTTTGCTACTCTTCCATCACAGCACCTAGGATGCTGG
TTGACTTGCTCTCAGGCAACCCTACCATTTCCTTTGGTGGATGCCTGACTCAACTCTTCTTC
15 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCATGGCGTATGACCGCTACA
TTGCCATTTCCCAGCCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT
ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC
AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTATTGTGATGTGCCTCAGCTGAT
CAAATTGGCCTGCACAGATACCTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG
20 GTGACCCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC
GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT
GGTGACCTTAATCTTTGTGCCTTGCATCTACGTCTATAACAAGGCCTTTTCGGACATTCCCCA
TGGACAAGGCCGTCTCTGTGCTATACAAATTGTCACCCCCATGCTGAATCCTGCCATCTA
TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG
ACCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

25

AOLFR43 sequences:

MQKPQLLVPIIATSNGLVHAAAYFLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE
RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIEFENICLAQMFLIHLSAVESAVLLA
MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFPLPFILKWLSCYQHTVTHSFLHQ
30 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRRAALKAFNTCISHLCV
LVFYVPLIGLSVHRLGGPTSLHVMANTYLLLPVNVNPLVYGAKTKEICSRVLCMFSSQGGK
(SEQ ID NO: 81)

35 ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG
CAGCATACTTCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT
TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATGTCTCATCAT
TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT
GACCTAGTCTCTCTCTATCACCATGCCCAAGATGGCCAGTCTTTCTGATGGCCATCCA
GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTTCCTTATCCATGCTGTGACCCGTG
40 GAGTCAGCTGTCCTGCTGGCCATGGCTTTTGACCGCTTGTGGCCATTGACCACCCATTGC
GCCATGCTTCTGTGCTGACAGGGGTGACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG
GGGGTTTGATTTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCTACTGCCAAACAC
ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC
CAGGGTCAATGTGGTTTATGGACTCTTCATCATCTCTCAGTCATGGGTGTGGACTCTCTCT
45 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCTCTCGGAGGGCA
GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC
CCTCATTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCCATGTGGTT
ATGGCTAATACCTACTTGCTGCTACCACCTGTAGTCAACCCCTTGTCTATGGAGCCAAGA
50 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID
NO: 82)

AOLFR44 sequences:

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFGNCIVVFIVRTERSLHAPMYLFLC
MLAAIDLALSTSTMPKILALFWFDSREISFEACLTQMFFIHLSAIESTILLAMAFDRYVAICHPL
55 RHA AVLNNVTVAQIGIVAVVRGSLFFPLPLLIKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP
NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLA FYVPLIGLS

VVHRFGNSLHPVIRVVMGDIYLLPPVINPIIYGAKTKQIRTRVLAMFKISCDKDLQAVGGK
(SEQ ID NO: 83)

5 ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA
AAGCCCATTTCTGGGTGGCTTCCCCCTCCTTCCATGTATGTAGTGGCAATGTTTGAAAC
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTC
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT
TCATGCCCTCTCAGCCATTGAATCCACCATCCTGCTGGCCATGGCCTTTGACCGTTATGTGG
10 CCATCTGCCACCCACTGCGCCATGCTGCAGTGTCAACAATACAGTAACAGCCAGATTGG
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC
TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA
GTTGGCCTATGCAGACACTTTGCCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTCTGC
15 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTGT
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAAACAGC
CTTCATCCCATTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA
TCCCATCATCTATGGTGCCAAAACCAAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG
ATCAGCTGTGACAAGGACTTGCAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

20

AOLFR45 sequences:

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA
MLATIDLVLSSSTLPKMLAIFWFRDQEINFFACLVMFFLHSFSIMESAVLLAMAFDRYVAICKP
LHYTTVLTGSLITKIGMAAVARAVTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRLACGDT
25 SFNNIYGIAMFVSVLDLLFVILSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS
SVMHRVARHAAPRVHILLAIIFYLLFPPMVNPIIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:
85)

30 TGGAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTGAACTCTAATCATATATA
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTTGTTGGTAGGAAT
TCCTGGTTTGGAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG
CCCTGCTAGGCAACTGTACCTTCTCTTCATTATCCAGGCTGATGCAGCCCTCCATGAACCC
ATGTACCTCTTTCTGGCCATGTTGGCAACCATTGACTTGGTCTTTCTTCTACAACGCTGCC
35 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC
CAGATGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGTGCTGCTGGCCATGGCCTT
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCCTGACTGGGTCCCTC
ATCACCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCT
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGTCTTCATCCT
TCAGGCAGTTCTCCAGCTTGCCTCTCAGGAGGCCCGCTACAAAGCATTGTTGGACATGTGTG
TCTCACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG
TGTAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC
45 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTTCGTGAGTATGTGCT
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT
ATCTTTGACAAATTCTAGTATGATAAGGAAAATGAGGTTTCATTCTCACAGATCTACGA
GTCAAGTCAAACCAGGAGTGCACCTATAGTCTGGTCTGATAGTAGGTTTGACCTTCCCA
50 TTGTCATAGACTACATCATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG
GGTGAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID
NO: 86)

AOLFR46 sequences:

55 MNIKHCGWHMIHTWLNIREDDDSDFKNFIGQIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHWV
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTTLLITIQLAS

LHQPLYLLSLLSLLDIVLCLTVIPKVLAIWFWDLRISFPACFLQMFIMNSFLTMESECTFMVMA
YDRYVAICHPLRYSIITDQFVARAVVFVIARNAFVSLPVMLSARLRYCAGNIKNICSNLSVS
KLSCDDITFNQLYQFVAGWTLLGSDLILIVISYFILKVVLRIKAEGAVAKALSTCGSHFILIFFS
TVLLVLVITNLARKRIPDPVILLNLHLIPALNPVYGVRTKEIKQGIQNLLKRL (SEQ ID NO:
5 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT
GATGACAGTGATTTTAAAACTTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC
10 TGGGTCTCCAGATTGATCANGAACTTTACATGGCATCTCCCAACAATGACTCCACTGCCC
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCCAACTTCCAGAGCTGGCAGCACTGGTTGTCT
CTGCCCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT
CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG
ACATCGTGTCTCTGCCTACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTGACCTCAGG
15 TCGATCAGCTTCCCAGCCTGCTTCTCCTCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA
TACCCGCTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA
ATGCCTTTGTTTCTCTTCTGTTCCCATGCTTTCTGCCAGGCTCAGATACTGTGCAGGAAAC
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAAACTCTCTTGTGATGACATCA
20 CTTTCAATCAGCTCTACCAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCTGATCTTATCCTT
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT
GGCCAAGGCCTTGAGCACGTGTGGTTCCCACTTCATCCTCATCCTCTTCTTCAGCACAGTCC
TGCTGGTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCCTCCAGATGTCCCCATCCT
GCTCAACATCCTGCACCACCTCATTCCCCCAGCTCTGAACCCATTGTTTATGGTGTGAGA
25 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

AOLFR47 sequences:

MSASNITLHTPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA
MLAAIDLVLSSALPKMLAIFWFRDREINFACLAQMFFLHFSFIMESA VLLAMAFDRYVAICK
30 PLHYTKVLTGSLITKIGMAAVARAVTLMTPLPFLLRFCFHYCRGPVIAHCYCEHMAVVRACGD
TSFNNIYGIAVAMFIVVLDLLLVILSYIFILQAVLLLASQEARYKAFGTCVSHIGAILAFYTTVVIS
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTTGGTGGGGATTCCAG
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG
CTTGAAACTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT
ACCTCTTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTCTCCTCCTCAGCACTGCCAAA
ATGCTTGCCATATTCTGGTTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCCA
40 TGTTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCCTCATCA
CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCTTCTCT
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG
45 CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATTCTTCAG
GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC
ATATAGGTGCCATCTTAGCCTTCTACAACTGTGGTCATCTCTTCACTCATGCACCGTGTA
GCCCCGCATGCTGCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC
CATGGTCAATCCCATATCTATGGTGTCAAGACCAAGCAATCCGTGAGAGCATCTTGGGA
50 GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFLPLCSLYLIAVLGNLTIIYIVRTEHSLHEPMYIFL
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH
55 PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNILSHSYCLHQDVMKLACDDI
RVNVVYGLVLIISAIGLDSLLISFSYLLILKTVLGLTREAAQAKAFGTCVSHVCAVFIFYVPFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLNPVYGVKTKEIRQLRLFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA
10 GATGTTTGGCCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCTTTT
GACCGCTATGTGGCCATCTGTCAACCCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG
TCACCAAAATTGGTGTGGCTGCTGTGGTGCAGGGGGGCTGCACTGATGGCACCCCTTCCTGT
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCTACTGCCTACACC
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT
15 CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA
AGACTGTGTTGGGCTTGACACGTGAAGCCAGGCCAAGGCATTTGGCACTTGCGTCTCTCA
TGTGTGTGCTGTGTTTCATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTC
GCAAGCGGCGTGACTCTCCGCTGCCCCGTCATCTTGCCAATATCTATCTGCTGGTTCCTCCT
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGCATCCTTCGA
CTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

AOLFR49 sequences:

MLTFHNVCSVPSSFWLGTGIPGLES�HVLSIPFGSMYLVA VVG NVTILAVVKIERSLHQPMYFF
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDACLGQMFLIHC FATVESGIFLAMAFDRYVAIC
NPLRHSMVLTYTVVGRGLVSLLRGVLYIGPLPLMIRLRLPLYKTHVISHSYCEHMAVVALTC
25 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKT LGTCASHLCAILIFYVP
IAVSSLIHRFGQCVPPP VHTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID
NO: 93)

30 ATGCTCACTTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG
GCTGGAGTCCCTACACGTCTGGCTCTCCATCCCCTTTGGCTCCATGTACCTGGTGGCTGTG
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG
TACTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA
ACTTCTGGGAATCTTCTGGTTCGGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA
35 ATGTTCCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCTTGCCATGGCTTTTGA
TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG
GGTCGTTTGGGGCTTGTCTCTCCTCCGGGTGTTCTCTACATTGGACCTCTGCCTCTGAT
GATCCGCTGTCGGCTGCCCTTTATAAAACCCATGTTATCTCCCACTCCTACTGTGAGCAC
ATGGCTGTATGTCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT
40 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATTTGCTGTTTCTTCCCTGATTACCG
ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAATTCTATCTCCTCATTC
CTCCAATCCTCAATCCCATTGTCTATGCTGTTTCGCACCAAGCAGATCCGAGAGAGCCTTCT
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

AOLFR50 sequences:

MNLSFFSFLLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFII
WMDPSLHQSMYLFSLMLAAIDL VVASSTAPKALAVLLVRAQEIGYTVCLIQMFTHAFSSMES
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLVRGLLLIPFLILLRKLIFCQATIIGHAY
50 CEHMAVVKLACSETTVNRAYGLTVALLVVGDLVLAIGVSYAHILQAVLVKVPNEARLKAFST
CGSHVCVILVFYIPGMFSFLTHRFGHHVPHHVLLAILYRLVPPALNPLVYRVKTQKIHQ
(SEQ ID NO: 95)

55 ATGAATTTGGATTCTTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC
CAGCTGGAGGCTACCCAGCCTTCTTTTTCTGCTAGGAATCCGGGTTTAGAGGAAAGC
CAGCACTGGATCGCACTGCCCTGGGCATCCTTACCTCCTTGCTCTAGTGGGCAATGTTA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGCACCAATCTATGTACCTCTTCCTGTCC
 ATGCTAGCTGCCATCGACCTGGTTGTGGCTCCTCCACTGCACCCAAAGCCCTTGCAGTGC
 TCCTGGTTCGTGCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTCACCCAT
 GCATTCTCCTCCATGGAGTCAGGGGTA CTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA
 5 TTTGTCACCCCCTGCACCATTCCACAATCCTGCATCCAGGGGTCATAGGGCACATCGGAAT
 GGTGGTGCTGGTGCGGGGATTACTACTCCTCATCCCCCTCCTCATTCTGTTGCGAAAACCTT
 ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAAC
 TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT
 TGGGCTGGATGTCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG
 10 GTACCAGGAAATGAGGCCCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTTGTGTCA
 TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTTCCTCACTCACCCTTTGGTCATCATGTA
 CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC
 TCTTGTCTATAGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM
 YIIALLGNTIIVTAIWMDSTRHEPMYCFCLCVLAAVDIVMASSVVPKMVSIFCSGDDSSISFSACFTQ
 MFFVHLATAVETGLLLTMAFDYVAICKPLHYKRILTPQVMLGMSMAITIRAIITPLSWMVS
 HLPFCGSNVVVHSYCEHIALARLACADPVPSSLYSLIGSSLMVGSDVAFIAASYILILKAVFGLSS
 20 KTAQLKALSTCGSHVGMALYLPGMASIYAAWLQGDVPLHTQVLLADLYVIIPATLNPIIY
 GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
 25 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTGGCTGGCTATCTCACTGA
 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
 CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
 30 CTGCTGCTGACCATTGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
 GAATTCTACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
 GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
 35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
 AGCATTAAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCAAAGTCCTGC
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC
 CAAACAAGTGCAGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
 40 CTGGGTTTCATGA (SEQ ID NO: 98)

AOLFR52 sequences:

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMDSTRHEPMY
 CFCLCVLAAVDIVMASSVVPKMVSIFCSGDDSSISFSACFTQMFFVHLATAVETGLLLTMAFDYV
 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMNMHLPFCGSNVVVHSYCKHIALAR
 LACADPVPSSLYSLIGSSLMVGSDVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGMALY
 YLPGMASIYAAWLQGDIVPLHTQVLLADLYVIIPATLNPIIYGMRTKQLLEGIWSYLMHFLFDH
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCCTCCTTGTGGGTA
 TCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC
 AGCCCTGTTAGGAAACACCCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC
 55 ACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG
 CTTTGTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA

AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTTCATGACTCCACTG
AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCTACTGTAA
GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG
ATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT
5 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAGCACATGT
GGCTCCCATGTGGGGGTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG
CCTGGTTGGGGCAGGATATAGTGCCCTTGACACCCCAAGTGTGCTAGCTGACCTGTACGT
GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAACAATTGCTGGAG
10 GGAATATGGAGTTATCTGATGCACTTCCTCTTTGACCACTCCAACCTGGGTTCATGA (SEQ
ID NO: 100)

AOLFR54 sequences:

MSDSNLSDNHLPDTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY
LFLCLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFCVHSIYALESSILLAMAFDRYVA
15 ICNPLRYTTILNHAIVIGRIGFVGLFRSVAIVSPFIFLLRRLPYCGHRVMTHTYCEHMGILARLACA
NITVNIVYGLTVALLAMGLDSILIAISYGFIHAFVHLP SHDAQHKALSTCGSHIGIILVFYIPAF
SFLTHRFGHHEVPKHVHIFLANLYVLVPPVLPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID
NO: 101)

20 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC
CAGGGCTGGAGGCTGCCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC
ACTGGTTGGAAATGCTGCCCTCATCTGGTTCATTGCCATGGACAATGCTCTTCATGCACCT
ATGTACCTCTTCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTTCTACCACTGTGCC
CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCTGGCC
25 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCGATTCTACTTGCCATGGCCTT
TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTCCTCAACCATGCTGTC
ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAGTGTGGCTATTGTCTCCCCCTTCATCTT
CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACATACTGTGAGCAT
ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG
30 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC
CATGCAGTCTTTACCTTCCATCTCATGATGCCAGCACAAGCTCTGAGTACCTGTGGCT
CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTCCTCACCCACCGC
TTTGGTCACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG
TGCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTCGGAGTCGACT
35 TCTAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

AOLFR57 sequences:

MSFQVTYMFYLHWTMEKSNNSTLFILLGFSQKNIEVLCFVLFYIAIWMGNLLIMISITCTQ
LIHQPMYFFLNYSLSDLCTSTVTPKLMVDLLAERKTISYNNCMQLFTTHFFGGIEIFILTM
40 AYDRYVAICKPLHYTHMSRQKCNTHIVCCTGGFIHSASQFLLTIFVPCGPNIDHYFCDEVYPLL
KLACSNHIMIGLLVIANGLIALVTFVLLSYVFILYTIRAYSAERRSKALATCSSHVIVVVLFF
APALFIYIRPVTTFSKDVLFYTHAPMFNPLIYTLRNTMKNAMRKVWCCQILLKRNQLF
(SEQ ID NO: 103)

45 ATGTCATTTAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA
GCACTTTGTTTATTCTCTTGGGGTTTTCCCAAATAAGAACATTGAAGTCTCTGCTTTGTA
TTATTTTTGTTTGCTACATTGCTATTGGATGGGAACTTACTCATAATGATTCTATCAC
GTGCACCCAGCTCATTACCAACCCATGTATTTCTTCTCAATTACCTCTCACTCTCCGACC
TTTGCTACACATCCACAGTGACCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC
50 CATTTCTATAATAACTGTATGATACAACTCTTACCACCCATTTTTTTGGAGGCATAGAGA
TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCTGCACTA
CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA
TTATACATTCTGCCAGTCAGTTTCTTCTCACCATCTTTGTACCATTTGTGGCCCAAATGA
GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA
55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG
TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA

5 AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCCTGCATTG
TTCATTTACATTAGACCGGTCACAACATTCTCAGAAGATAAAGTGTTTGCCCTTTTTTATAC
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC
GCCATGAGGAAAGTGTTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ
ID NO: 104)

AOLFR58 sequences:

10 MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQPNPVQEIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

15 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCCTTGGATGTACCAACTTGTTAA
TGACTATGATACCAAAATTGATCTGAAGCAAATTTTCTTTGTCTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTGGGACTTTCACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTTCTC
20 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGTCTTCTGGA
TGCCTGCTTCTCATCTGTCTACACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTGCAAGCCCTTGCA
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
25 GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGCTGTCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG
GAAAGCTCTCTCCACCTGTGGATCTCAGATTGCTGTTGTGATTTTGTCTTTGTCCTCATGCA
30 TATTTGTATATACAGCACTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCTTTGATTACACTTTCAGGAATAAGGAAGTAAAC
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 106)

35 **AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGLLEYVHSWLSILFCLAYLVAFMGNVTILSVIWISSLHQPMYYFI
SILAVNDLGMSTLPTMLAVLWDAPEIQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH
PLHYTILTNSVIGKIGLACLLRSLGVVLPPLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA
RTNSYGLCVVIATLGVDSIFILLSYVLIINTVLDIASREEQLKALNTCVSHICVVLFFVPVIGVS
40 MVHRFGKHLSPIVHILMADIYLLLPVLPVIVSVRTKQIRLGILHKFVLRRLF (SEQ ID NO:
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTG
GACTGGAGTATGTTTCACTTCTGGCTCTCCATCCTCTTCTGTCTTGCATATTTGGTAGCATTT
45 ATGGGTAATGTTACCATCCTGTCTGTCAATTGGATAGAATCCTCTCTCCATCAGCCCATGTA
TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCACCA
TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT
GTTCTTCATCCACACATTCACATTCCTGGAGTCTCAGTGTTGCTGGCCATGGCCTTTGACC
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCAACAGTGTAATTGGC
50 AAAATTGGTTTGGCCTGTTTGTACGAAGCTTGGGAGTTGTACTTCCACACCTTTGCTACT
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTCACGCCTTCTGTTTGCAACCAGGAT
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCTTTGTGTAGTCA
TTGCCACACTAGGTGTGGATTCAATCTTCATACTTCTTTCTTATGTTCTGATTCTTAATACT
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCAT
55 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG
AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT

CCTTAACCCTATTGTCTATAGTGTCAGAACAAAGCAGATTCGTCTAGGAATTCTCCACAAG
TTTGTCCCTAAGGAGGAGGTTTAA (SEQ ID NO: 108)

AOLFR60 sequences:

5 MFLPNDTQFHPSSFLLGIPGLETLHIWIGFPFCVYMIALIGNFTILLVIKTDSSLHQPMFYFLA
MLATTDVGLSTATIPKMLGIFWINLRGIIFEACLTQMFFIHNFTLMESAVLVAMAYDSYVAICN
PLQYSAILTNKVVSIGLVFVRALIFVIPSILLILRLPFCGNHVIPHTYCEHMGHLHLSCASIKINI
IYGLCAICNLVFDITVIALSYVHILCAVRLPHEPRLKSLSTCGSHVCVILAFYTPALFSFMTHC
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF
10 (SEQ ID NO: 109)

ATGTTCCCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC
ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCATGT
15 TCTACTTCTGGCCATGTTGGCCACCACTGATGTGGGTCTCTCAACAGCTACCATCCCTAA
GATGCTTGGAATCTTCTGGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG
ATGTTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTGT
TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCAATCCCTCTATACTTC
20 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCACACACCTACTGTGAGCACAT
GGGTCTTGCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTTATGGTTTATGTGCCA
TTTGTAACTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT
GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT
GTGTGTAATCCTTGCCTTCTATACACCAGCCCTCTTTTCTTTATGACTCATTGCTTTGGCC
25 GAAATGTGCCCCGCTATATCCATATACTCCTAGCCAATCTCTATGTTGTGGTGCCACCAAT
GCTCAATCCTGTCATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT
ATTATTGCAGGAACAAGGAATGGAAGGAAGAGTACCTAATACATACGAGGTTCTGA
(SEQ ID NO: 110)

AOLFR61 sequences:

30 MSIINTSYVEITTFVLVGMPPLEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHGPMYYFLSML
AMSDLGLSSLPTVLSIFLNPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT
SILTTVRVAQIGIVFSFKSMLLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEELKALNTCVSHICAVIIFLPIINLAVVHRFAG
35 HVSPLINVLMAINVLLLVPLMKPIVYCVKTKQIRVRVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
40 CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCATGT
ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTTAAGCATCTTCCCTGTTCAATGCCCTGAAACTTCTTCTAGTGCCTGCTTTGCCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTTGATA
GATTCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGTCCTGTTCTTCCCTTCCCTTTCACTT
45 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT
ACCGGGAATTGCATCCAAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC
TGTCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
50 GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA
TGAAACCAATTGTTTATTGTGTAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

AOLFR62 sequences:

55 MFYHNKSIFHPVTFFLIGPLEDFHWMISGPFCSVYLVALLGNAITILLVIKVEQTLREPMFYFL
AILSTIDLALSATSVPRMLGIFWFDAHEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC

APLHYATILTSVLVVGISMCIIVIRPVLLTLPVMVYLIYRLPFCQAHIIAHSYCEHMGIAKLSCGNIRI
NGIYGLFVVSFFVLNLVLIGISYVYILRAVFRLP SHDAQLKALSTCGAHVGVICVFYIPSVFSFLT
HRFGHQIPGYIHILVANLYLIIPPSLNPYIYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

5 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCCTCATTGGAATCCCAGG
TCTGGAAGACTTCCACATGTGGATCTCCGGGCCCTTCTGCTCTGTTTACCTTGTGGCTTTGC
TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT
CTACTTCCTGGCCATTCTTTCCACTATTGATTGGCCCTTCTGCAACCTCTGTGCCTCGCA
TGCTGGGTATCTTCTGGTTTGATGCTCACGAGATTAACATATGGAGCTTGTGTGGCCAGAT
10 GTTCTGATCCATGCCTTCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC
CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT
GGGCATTAGCATGTGCATTGTAATTCGTCCCGTTTTACTTACACTTCCCATGGTCTATCTTA
TCTACCGCCTACCTTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG
CATTGCAAAATTGTCCTGTGGAACATTTCGTATCAATGGTATCTATGGGCTTTTTGTAGTTT
15 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC
TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG
GAGTCATCTGTGTTTTCTATATCCCTTCAGTCTTCTTTTCTTACTCATCGATTTGGACAC
CAAATACCAGGTTACATTACATTCTTGTGCAATCTCTATTTGATTATCCCACCTCTCT
CAACCCCATCATTTATGGGGTGAGGACAAACAGATTCGAGAGCGAGTGCTCTATGTTTTT
20 ACTAAAAAATAA (SEQ ID NO: 114)

AOLFR63 sequences:

MSIINTSYVEITTFVLVGMPLGEYAHIWISIPICSMYLIAILGNGTILFIKTEPSLHEPMYYFLSML
AMSDLGLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYTS
25 ILTTVRVAQIGIVFSFKSMMLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY
GFFGALCLMVDFILIAVSYTLILKTVLGIASKKEQLKALNTCVSHICAVIIFYLPINLAVVHRFAR
HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLCQRKI (SEQ ID NO: 115)

ATGTCCATTATCAACACATCATATGTTGAAATCACCACCTTCTTCTTGGTTGGGATGCCAG
30 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT
CTAGGAAATGGCACCATTCTTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT
ACTATTTTCTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT
GTGTAAAGCATCTTCCTGTTCAATGCTCCTGAAATTCATCCAATGCCTGCTTTGCCCAGGA
ATTCTTCATTCATGGATTCTCAGTACTGGAGTCTCAGTCTCCTGATCATGTCAATTTGATA
35 GATTCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT
TAAGAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCTGATCCTCAAGACTGT
40 ACTGGGAATTGCATCCAAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTACACATC
TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCCG
GCATGTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA
CGAACCCAATTGTTTATTGTGTAAAAACTAAACAGATTAGAGTGAGAGTTGTAGCAAAATT
GTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

45

AOLFR64 sequences:

MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTVLGNLTILHVICTDATLHGPMYYFLG
MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL
HDSTVLTPACIVKMGLSSVLRALLILPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVN
50 HIYGLFVVACTVGVDSSLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV
HRFGEHLPRVVHLFMSYVYLLVPPLMNPIIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID
NO: 117)

ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG
55 GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC
TTGGGGAACCTCACCATTCTCCACGTCATTTGTACTGATGCCACTCTCCATGGACCCATGT

ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCCACT
 GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC
 TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC
 CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCCTGACACCTGCATGTATTG
 5 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCCTTGCCATTCTC
 CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA
 GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG
 GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATAACGCCCTCATCCTTCGCAC
 CGTGCTCAGCATTGCCTCCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT
 10 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG
 TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCCTATGTGTATCTGCTGGTACCACCCC
 TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAGAA
 GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNTQFHPSSFLLLGIPGLEDVHIWIGVPPFFVYLVALLGNTALLFVIQTEQSLHEPM
 YYFLAMLDSIDLGLSTATIPKMLGIFWNTKEISFGGCLSHMFFIHFFTAMESIVLVAMAFDRI
 AICKPLRYTMILTSKIISLIAGIAVLRSLYMVVPLVFLLLRPFCHRIIPHTYCEHMGARLACAS
 IKVNIRFGLGNISLLLDVILIILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL
 20 THRFGHNIPQYIHILANLYVVVPPALNPVIYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCTACTGCT
 GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTTCTTTGTGTAT
 CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC
 25 ATGAGCCTATGTACTACTTCTGGCCATGTTGGATTCCATTGACCTGGGCTTGTCTACAGC
 CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTGGAGGC
 TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC
 CATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA
 GCAAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTCC
 30 ACTGGTGTCTCTCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT
 GTGAGCACATGGGCATTTGCCGCTGTGCCAGCATCAAAGTCAAACATTAGGTTTGG
 CCTTGGCAACATATCTCTCTTGTATCGGATGTTATCCTTATTATTCTCTCCTATGTCAGGA
 TCCTGTATGCTGTCTTCTGCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGT
 GGTTCTCATATTGGTGTTATCTTAGCCTTTTTTACACCAGCATTTTTTTTCATTCTTGACACA
 35 TCGTTTTGGCCATAATATCCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG
 TCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTTCGAGAGAGAG
 TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

AOLFR66 sequences:

40 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL
 ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMMLMALDHCVAI
 CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN
 VRVNAIYGLIVALLIGGFDILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF
 TFFTHHFGGHTIPLHIHIIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ
 45 ID NO: 121)

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTATCCTAAATGGCATCCCTG
 GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCAGTGTGTACCATGTACAGCATTGCTATT
 ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT
 50 ATGCTCTCCTTGCCCTTCTTTCTTACAGATGTGCTCATGTGCACCAGCACCCCTTCCCAAC
 ACTCTCTTCATATTGTGGTTAATCTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCCAGAT
 GTTCTTTGTGCACACCTTACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGAC
 CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGC
 TAAAGCTGGGTTCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCTCTCA
 55 CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC
 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC
 AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCCAC
 TTCTGTGCCATAGTCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCAATTTGG
 GGGACACACCATTCCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC
 5 CCACAATGAACCCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAGTGTCTTA
 GGTTCCTTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

AOLFR67 sequences:

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIAVVGNCGLICLISHEEALHRPMMYYFLA
 10 LLSFTDVTLCCTTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVMLMALDRYVAI
 CYPLRYATILTNPVIAKAGLATFLRNVMLIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN
 FKVNAIYGLMVALLIGVFDICCSVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF
 FTFTHRFVGHNPNIHIIIVANLYLLPPTMNPVYGVKTKQIQEGVIKFLLDGDKVSFTYDK
 (SEQ ID NO: 123)

15 ATGTCTGGGGACAACAGCTCCAGCCTGACCCCAGGATTCTTTATCTTGAATGGCGTTCCTG
 GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTGCTGTC
 GTGGGGAACCTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT
 ACTACTTCCTGGCCCTGCTCTCCTTCACTGATGTACCTTGTGCACCACTATGGTACCTAAT
 20 ATGTCTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCGAGA
 TGTTTTGTGCCATATGCTGACAGGGATGGAGTCTGGGGTGCTCATGCTCATGGCCCTGGA
 CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG
 CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCCATTCCTCTCCTC
 25 ACCAAGCGCTGCCCTATTGCCGGGGAACTTCATCCCCACACCTACTGTGACCATATGT
 CTGTGGCCAAGGTATCCTGTGGCAATTTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC
 TCTCCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG
 CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA
 CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTGT
 30 AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT
 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTGAGGAAGGTGTAATTA
 AATTTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

AOLFR68 sequences:

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTTLLMTIWLEASLHQPL
 35 YYLLSLLSLLDIVLCITVPKVLITWFDFLRPISFPACFLQMYIMNCFAMESCTFMVMAYDRY
 VAICHPLRYPSTHDHFVKAAMFILTRNVMLTPIPILSAQLRYCGRNVIENCICANMSVSRISC
 DDVTINHLIYQFAGGWTLGSDLILIFLSYTFILRAVLRLKAEGAVAKALSTCGSHFMLILFFSTIL
 LVFVLTHVAKKKVSPDVPVLLNLVHHVIPAALNPIIYGVRTQEIKQGMQRLLKKGC (SEQ ID
 NO: 125)

40 ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT
 TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCTCAGCCTCCTTTTCTCTTG
 GCCGTAGGGGGCCAACACCACCCTCCTGATGACCATCTGGCTGGAGGCCTCTCTGCACCAGC
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC
 45 CCCAAGGTCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCCT
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGACATTTCATGGTTCATGGCC
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT
 TGTAAGTCAAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC
 50 ATCCTTTCAGCACAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA
 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCCTACACCTTCATTCT
 GCGAGCTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG
 CTCCCACTTCATGCTCATCCTCTTCTTTCAGCACCATCCTTCTGGTTTTTGTCTCACACATGT
 55 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT
 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCAAGAAATTAAGCAGGGGAATG
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

AOLFR69 sequences:

MSYSIYKSTVNIPLSHGVVHSFCHNMNCNFMHIFKFVLDFNMKNVTEVTLFVLKGFTDNLELQ
TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN
5 KVISFLGCVAVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVSMSPRVYMPINASYVAGI
LHATIHTVATFSLFCGANEIRRVFC DIPLLAISYSDHTNQ LLLFYFVGSIELVTILIVLISYGLIL
LAILKMYS AEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHD MIVSIFYTIVIPLLNPV
IYSLRNKDVKDSMKMFGKNQVINKVYFHTKK (SEQ ID NO: 127)

10 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT
CTTTTTGTCATAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC
ATGAAGAATGTCACCTGAAGTTACCTTATTTGTAAGGAGGCTTCACAGACAATCTTGAAC
TGCAGACTATCTTCTTCTTCTGTTTCTAGCAATCTACCTCTTCACTCTCATGGGAAATTTA
GGACTGATTTTAGTGGTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA
15 GTATGTTGTCTTCTGTGGATGCCTGCTATTCCTCAGTTATTACCCCAAATATGTTAGTAGAT
TTTACGACAAAGAATAAAGTCATTTTCATTCTTGGATGTGTAGCACAGGTGTTTCTTGTCT
GTAGTTTGGAAACCACAGAATGCTTCTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC
CATCTACAACCTCTCCTGTATTCACTGAGCATGTCACCCAGAGTCTACATGCCACTCATC
AATGCTTCCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT
20 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTTGTGATATCCCTCCTCTCCTTGCTA
TTTCTTATTCTGACACTCACACAAACCAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG
CTGGTCACTATCCTGATTGTTCTGATCTCCTATGGTTGATTCTGTTGGCCATTCTGAAGAT
GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT
GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTCCAGCTATGCTTCG
25 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCCTTGCTGAATCCCCTCAT
CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA
GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

AOLFR70 sequences:

30 MDSTFTGYNLYNLQVKTEMDKLSSGLDIYRNPLKNKTEVTMFILTGFTDDFELQVFLFLFFAI
YLFTLIGNLGLVVLVIEDSWLHNP MYFLSVLSFLDACYSTVVT PKMLVNFLAKNKSISFIGCA
TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVSMSPRVYVPLITASYVAGILHATIHIVA
TFSLSFCGSNEIRHVFC DMPLLAISCSDHTNQ LLLFYFVGSIEIVTILIVLISCDFILLSILKMHSA
KGRQKAFSTCGSHLTGV TIYHGTILVSYMRPSSSYASDHD IIVSIFYTIVIPKLNPIIYSLRNKEVK
35 KAVKKMLKL VYK (SEQ ID NO: 129)

40 ATGGACTCCACTTTCACAGGCTATAACCTTTATAACCTGCAAGTAAAAACTGAAATGGACA
AGTTGTCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA
TGTTTATATTGACAGGCTTCACAGATGATTTT GAGCTGCAAGTCTTCCTATTTTTACTATTT
TTTGCAATCTATCTCTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG
ATTCTGCTCCACAACCCCATGTATTATTTTCTTAGTGTTTTATCATTCTTGGATGCTTGC
TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGCGCAAAAAATAAATCCATT
CATTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT
CTCTTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCCCTCCTGTATTCACT
45 GAGCATGTCAACCAGAGTCTATGTGCCACTCATCACTGCTTCCTACGTTGCTGGCATTTTAC
ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG
GCATGCTTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC
AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCTCATT
TCCTGTGATTTTATTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG
50 CCTTCTCTACATGTGGCTCTCACCTAACTGGAGTGACAATTTATCATGGAACAATTCTCGTC
AGTTATATGAGACCAAGTCCAGCTATGCTTCAGACCATGACATCATAGTGTCAATATTT
ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGAAGTAAA
AAAGGCAGTGAAGAAAATGTTGAAATTGTTTACAAATGA (SEQ ID NO: 130)

AOLFR71 sequences:

MGRNRNTNVPDFILTGLSDSEEVQMALFILLLIYLITMLGNVGMILIIRLDLQLHTPMYFFLTH
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLLSSMAYDRYVAICSPRLY
PVIMSKRLCCALVTGPYVISFINSFVNVVWMSRLHFCDSNVVRHFFCDTSPILALSCMDTYDIEI
5 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVTIFYGTMIFTYLPKPRK
SYSLGRDQVASVIFYTIVIPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC
10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTTT
TCCTTACTCACTTGTTCATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAACCTTA
GCGAACTTACTGACTTCCAACATATTTTCCTTCATGGGCTGCTTTGCCAGATGTTCTTTTT
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG
CTATCTGCAGTCCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC
15 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC
TGCATTTCTGCGACTCAAATGTAGTTCGTCACCTTTTTCTGCGACACGTCTCCAATTTTAGCT
CTGTCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCACCC
TGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCTGAAA
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG
20 TCACCATCTTTTATGGAACATGATTTTTACTTATTTAAACCAAGAAAGTCTTATTCTTTG
GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT
TTATAGTCTTAGAAACAAAGAAGTTAAAAATGCTCTCATTAGAGTCATGCAGAGAAGACA
GGACTCCAGGTAA (SEQ ID NO: 132)

AOLFR72 sequences:

MAPENFTRVTEFILTVGVSSCPQLIPLFLVFLVLYGLTMAGNLGHITLTSVDSRLQTPMYFFLQHL
ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL
YMVVVSRRLLCLLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFCYDNVPLALSCSDTYLPE
TVVFISAAATNVVGSLLIIVLVSYFNIVLSILKICSSEGRKKAFTSCASHMMAVTIFYGTLLFMYVQP
30 RSNHSLDTDKMASVFYTLVIPMLNPLIYSLRNKDVKLTALQRFMTNLCYSFKTM (SEQ ID NO:
133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC
CAGAGCTCCAGATTCCCCTCTTCCTGGTCTTTCTGGTGTCTATGGGCTGACCATGGCAGG
35 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCCATGTACTTTT
TCCTGCAACATCTGGCTCTCATTAATCTTGGTAACTCTACTGTCATTGCCCTAAATGCTG
ATTAACCTTTTAGTAAAGAAAGAAACTACCTCATTCTATGAATGTGCCACCAACTGGGAG
GGTCTTGTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT
GTGGCTATTTGTAACCCCTCTGCTGTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGCT
40 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT
CTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATAATGTTCTCTGTTA
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA
ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTTGTCTATTTTA
AAAATATGTTTCATCAGAAGGAAGGAAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG
45 CAGTCACAATTTTTTATGGGACATTGCTATTCTATGTATGTGCAGCCCCGAAGTAACCATTC
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT
CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTCATGACA
AATCTGTGCTATTCTTTAAACAATGTAA (SEQ ID NO: 134)

AOLFR73 sequences:

MNHVVKHNHTAVTKVTEFILMGITDNPLQAPLFLFLIYLVTVIGNLGMVILTYLDSKLHTP
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISSELFILSAMAYDRYV
AICKPLLYVIIMAEKVLWVLVIVPYLYSTFVSLFTIKLFKLSFCGSNIISYFYCDCIPLMSILCSDT
NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVMIMFYGTLLFIYL
55 QPKSSHTLAIDKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA
 CACACCCCATGTACTTTTTCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT
 5 CATTGCCCCGAAGATGTTAGTAAACTTCATAGTGACAAAAACACAATTTCTTACAATTGG
 TATGCCACTCAGCTAGCATTTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACATTT
 TCTCACAATTAAGTTATTTAAACTGTCCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT
 10 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT
 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTTACTTGCA
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCCTGTTG
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAGATGCTCTAA
 AGAGAACTTTAACCAATCGATTCAAAATTCCCATTAA (SEQ ID NO: 136)

AOLFR74 sequences:

20 MEQHNLTTVNEFILTGITDIAELQAPLFALFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH
 LAFMDLGYSTTVGPKMLVNFVVDKNISYFYCATQLAFLVFIGSELFILSAMSVDLYVAICNPL
 LYTVIMSRRCVQLVAIPYLYCTFISLLVTIKIFTLSCGYNVISHFYCDLPLPLLCNSNTHIEILI
 ILIFAAIDLISLLIVLLSYLLILVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMVYQPKSSH
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

25 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC
 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCCCTCATGATCTATGTGATCTCAGTGATGG
 GCAATTTGGGCATGATTGTCCTCACCAAGTTGGACTCCAGGTTGCAAACCCCTATGTACTT
 TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACGTGGGGACCCAAAATG
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTGTGCAACACAGCTAGC
 30 TTTCTTTCTTGTGTTCACTGGTAGTGAACCTTTTATTCTCTCAGCCATGTCCTACGACCTCT
 ATGTGGCCATCTGTAAACCCTCTGCTATACACAGTAATCATGTGCAGGAAGGTATGTCAGGT
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCAATTTCTCTTCTAGTCACCATAAAGATTT
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGTCTCCCTTTG
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT
 35 TGATTTGATTTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT
 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCCACCTGACAGTG
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCTT
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCATGTTGAATCCCTTGA
 TCTATAGTTTACGAAACAAAGATGTAAATATGCCCTACGAAGGACATGGAATAACTTATG
 40 TAATATTTTGTTTAA (SEQ ID NO: 138)

AOLFR75 sequences:

MEGKNQTNISEFLLLGFWQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLA
 NLSLVDLCLPSATVPKMLLNITQTQTISYPGCLAQMYFCMMFANMDNFLTVMAYDRYVAI
 45 CHPLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMMAHLHFCSDNVIIHFFCDINSLLPLSCSD
 TSLNQLSVLATVGLIFVPSVILVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT
 GVYMSPLSNHSTEKDSASVIFMVVAPVLNPFYSLRNELKGTLLKTLRPGAVAHACNPSTL
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC
 AACAACAGCAGGTGCTACTCTTTGCACTTTTCTGTGTCTCTATTAAACAGGGCTGTTTGA
 AACTTACTCATCTTGTGGCCATTGGCTCGGATCACTGCCTTCACACACCCATGTATTTCTT
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT
 55 CTGTATGATGTTTGCCAATATGGACAATTTCTTCTCACAGTGATGGCATATGACCGTTAC
 GTGGCCATCTGTCAACCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT

GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCCTCTCTTGCACACTCTTATGATGGCCC
 ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTTCTTCTGTGATATCAACTCTCTCCTC
 CCTCTGTCTGTTCCGACACCAAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA
 TCTTTGTGGTACCTTCAAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG
 5 AAAGTCCCTTCTGCCCCAAGGAAAACCAAGGCTTTCTCTACCTGTGGATCTCACCTTGCCTT
 GGTCATTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCTTATCCAATCACTCT
 ACTGAAAAAGACTCAGCCGCATCAGTCATTTTTATGGTTGTAGCACCTGTGTTGAATCCAT
 TCATTTACAGTTTAAAGAAACAATGAACTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC
 CGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA
 10 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

AOLFR76 sequences:

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILILLDSHLHTPMYFFLSNLSLA
 GIGYSSAVTPKVLTLGLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY
 15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL
 VLISSFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM
 DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA
 20 CTACAGGTTCCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT
 GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTAATTTTTTCTCA
 GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG
 GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTGT
 GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG
 25 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGTGCTTGTCTGGC
 TATAGGCTGTTATGTCAATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTGCC
 TCTCTTTCTGCATGTCCAATGTGATTTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT
 CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTTAATGT
 CTTTTTGCACCTCTTGTACCTTGATTTCCTATCTGTTCATATTGATCACCATTCTTAAGAG
 30 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT
 TTCTTATTTATATACTGTACATCATGTACATACGACCAAGTTCCAGTCATTCCATGGA
 CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT
 ATACCCTGAGGAACAAAGACGTGAAGAATGCATTTCATGAAGGTTGTTGAGAAGGCAAAAT
 ATTCTCTAGATTCAGTCTTTTAA (SEQ ID NO: 142)

AOLFR77 sequences:

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS
 QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTMGVAEGVLLVMSYDRYVAVC
 QPLQYPVLMRRQVCLLMGSSWVGVNLASIQTSLTHFPYCASRIVDHFFCEVPALLKLSCA
 40 DTCA YEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGFLFYGA
 AVFMYMVP CAYHSPQQDNVVS L FYSLV TPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC
 (SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT
 45 CAGGATCACGCCAGTCCCTCTTCTCCCTGGTGGCTGTGTCATGTTGTGATAGGCCTTCTGGGC
 AACACCGTTCTTCTCTTCTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTAATTCCT
 GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA
 TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT
 TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA
 50 TGTGCTGTGTGCCAGCCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG
 ATGATGGGCTCCTCCTGGGTGGTAGGTGTGCTCAACGCCTCCATCCAGACCTCCATACCC
 TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA
 CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC
 TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT
 55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTACACCTGCTCCTCGCACATCA
 CGGTAGTGGGGCTCTTTATGGTGCCGCGGTGTTTCATGTACATGGTGCCTTGCAGCTACCA

CAGTCCACAGCAGGATAACGTGGTTTTCCCTCTTCTATAGCCTTGTCACCCCTACACTCAAC
CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTGGTCAAAGTGCTTAGCA
GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF
FLGNLSCLEILLTSVIIPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH
PLRYPLLLMSGAVCFRVALACWVGGLVPVLGPTVAVALLPFCCKQGAUVVQHFFCDSGPLRLAC
TNTKKLEETDFVLASLVIVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI
10 FLYVRPSQSGSVDTNWAVTVITTFVTPLLNPFYIALRNEQVKEALKDMFRKVVAGVLGNLLD
KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA
AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT
15 GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT
GTACTTCTTTCTGGGTAACCTGTCCTGCCTAGAGATACTGCTCACTTCTGTGCATCATTCCAA
AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCATGTATCACCCA
ATTCTATTTCTACTTCTTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGCATGTCTGCGG
ATCGCTACCTGGCCATCTGTATCCTCTGCGCTACCCCTGCTCATGAGTGGGGCTGTGTG
20 CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGACTCGTCCCTGTGCTTGGTCCACAGTG
GCTGTGGCCTTGCTTCTTTCTGTAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA
GTGGCCCACTGCTCCGCCTGGCTTGACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT
CCTGGCCTCCCTCGTCATTGTATCTTCTTGTGCTGCTGCTGTGCTTACGGCCTCATTG
TGCTGGCAGTCTGAGCATCCCCTCTGCTTCAGGCCGTCAGAAGGCCTTCTCTACCTGTAC
25 CTCCCACTTGATAGTGGTGACCCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT
CGCAGAGTGGTTCTGTGGACACTAAGTGGGAGTGCAGTAATAACGACATTTGTGACAC
CACTGTTGAATCCATTCTATGCCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA
CATGTTTAGGAAGGTAGTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT
GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

30

AOLFR79 sequences:

MTPGELALASGNHTPVTKFILQGFSNYPDLQELLFGAILLIYAITVVGNLGMMLIFTDSHLQSP
MYFFLNVLSDLICYSSVTPKLLVNFLVSDKSISFEGCVVQLAFFVVHVTAESFLLASMAFYDR
FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANSIAITGNVFALPFCGPNQLTHYYCDIPPLH
35 LACANTATARVVLVVSALVTLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI
FYGTVVFTYVQPHGSTNNTNGQVVSFYTIIIPMLNPFYSLRNKEVKGALQRKLQVNIFPG
(SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGGCAACCACACCCAGTCACCAAGTTCATCT
40 TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCCTGCTCAT
CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT
CTCCAAAGCCCAATGTATTTCTTCTCAATGTCTCTCGTTTCTTGATAATTTGTTACTCTTCT
GTGGTCACACCTAAGCTCTTGGTCAACTTCTGCTCTGACAAGTCCATCTCTTTGAGG
GCTGTGTGGTCCAGCTCGCCTTCTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC
45 CTCCATGGCCTATGACCGCTTCTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA
CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGCTCATGCATTTGGTGGAGCCAACTCCGC
TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCAACCAGCTAACACACTAC
TACTGTGACATAACACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG
TCCTCTATGTCTTTTCTGCTCTGGTCAACCTTCTGCTGCTGCAGTCATTCTCACCTCCTACT
50 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT
CCACTTGTGCCTCCCACTTTCTGGCCATTGCCATTTCTATGGCACTGTGGTTTTACCTAT
GTTTACGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA
TCATAATTCCCATGCTCAATCCCTTCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC
TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

55

AOLFR80 sequences:

MEGINKTAKMQFFFRPSPDPEVQMLIFVVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA
NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH
PLRYRLIMSWSLCVELLVGSVLGFLSLPLTILIFHLPFCHNDEIYHFYCDMPAVMRLACADTR
5 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHLVLLQYGCTSFIVLSPS
SSYSPEMGRVVSVAITYFITPILNPLIYSLRNKELKDALRKALRK (SEQ ID NO: 149)

ATGGAAGGAATAAATAAACTGCAAAGATGCAGTTTCTTTCGTCCATTCTCACCTGACC
CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGTATCTGACCAGCCTCGGTGG
10 AAATGCTACAATTGCAGTCATTGTTGAGATCAATCATTCCCTCCACACCCCCATGTACTTTT
TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCATTGGCCTTG
GCAAACCTCCTTTCAATGGGCAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT
TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTCTGCTGGTAGTCATGGCTTATGACCGG
TTTATAGCGATCTGTCAACCCTCTGCGATACAGGCTCATCATGAGCTGGTCCTTGTGTGTGG
15 AGCTGCTGGTAGGCTCCTTGGTGCTGGGGTTCTGTTGTCACTGCCACTCACCATTTTAATC
TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCACTTCTACTGTGACATGCCTGCAGT
CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC
ATCGTCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT
TTTACGGATCCGGTCAGCAGAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC
20 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTTCCAGCTA
CTCTCCTGAGATGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC
CCCTTGATCTATAGTTTGAGGAACAAGGAAGTGAAGATGCCCTAAGGAAAGCATTGAGA
AAATTCTAG (SEQ ID NO: 150)

AOLFR81 sequences:

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS
LSFLDFCYSSVITPKMMKLWMESHLIVPETRPSRMSNQTLVTEFILQGFSEHPEYRVFLFSCF
LFLYSGALTGNVLITLAITFNPLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC
MAQLYFLTWAASSELLLLVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH
30 TGLMLRLDFCGPNVIIHFFCEVPPLLLSCSSSTYVNGVMIVLADAFYGIVNFLMTIASYGIVSSI
LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL
IYTLRNKEVKAAALRKLFPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG
ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT
ACCGGGTGTCTTATTAGCTGTTTCCTCTTCTCTACTCTGGGGCCCTCACAGGTAATGTC
CTCATCACCTTGGCCATCACGTTCAACCCTGGGCTCCACGCTCCTATGTACTTTTCTTACT
CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCAAGCGCTGGCCAGT
CTGGTGTGCGGAAGAGAGCTCCATCTCCTACGGGGCTGCATGGCCAGCTCTATTTCTCA
40 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTGCATGGCCATGACCGGTACGCAGC
CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC
ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT
TGGATTTCTGTGGCCCCAATGTCAATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT
CTCTCCTGCAGCTCCACCTACGTCAACGGTGTGATGATTGTCCTGGCGGATGCTTTCTACG
45 GCATAGTGAACCTTCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA
GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG
GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG
CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCCTCAACCCCT
CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC
50 AGAAATTAA (SEQ ID NO: 152)

AOLFR82 sequences:

MQLNNNVTEFILLGLTQDPFWKKIVFVIFLRLYLGTLLGNLLIIISVKASQALKNPMFFFLFYLSL
SDTCLSTSIAPRMIVDALLKKTISFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII
55 SQWVCGVLMVAWVGSCVHSLVQIFLALSPLFCGPNVINHCFCDLQPLLKQACSETYVNNLL

VSNSGAICAVSYVMLIFSIVFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP
MDKMIAVFYTVGTSFLNPVIYTLKNTEVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT
GGAAGAAAATAGTGTGTTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAATTT
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCCTT
TTCTACTTATCTTTATCTGATACTTGCCCTCTCTACTTCCATAGCCCCTAGAATGATTGTGGA
TGCCCTTTTGAAGAAGACAACACTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC
10 CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA
CATCTGTAAGCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTTGTG
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTTCTTGCCCTGAGTTT
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTGAAA
CAAGCCTGTTCAGAAACCTATGTGGTTAACTACTCCTGGTTTCCAATAGTGGGGCCATTT
GTGCAGTGAGTTATGTGCTAATATTCTCCTATGTGCTCTCTTGCAATTCTCTGAGAAAC
15 CACAGTGCTGAAGTGATAAAGAAAGCACTTCCACATGTGTCTCCACATCATTGTGGTCA
TCTTGTTCTTTGGACCTTGCAATTTATGTACACATGCCCTGCAACCGTATTCCTCATGGAT
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCCTGTGATTTACACGCT
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA
TGACAAAAGATAA (SEQ ID NO: 154)

20

AOLFR83 sequences:

MGNWTAADVTEFVLLGFSLSREVELLLLVLPTFLLTLLGNLLIISTVLSLRLHTPMYFFLCNL
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFLGTVEFLLLTVMYSYDRYATICPLRYT
TIMRPSVCIGTVVFSWVGFLSVLFTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF
25 MLSSMVILCCIVLVAYSITYIILTIVRIPSASGRKKAFTNCASHLTIVIIPSGITVFIYVTPSQKEYL
EINKIPLVLSSVVTPLNPFYTLRNDTVQGVLRDVWVRVGRGVFEKRMRAVLRSLSSNKDQ
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCCACGTTCTGCTGACTCTTCTGGGGAA
CCTGCTCATCATCTCCACTGTGCTGTCCTGCTCCCGCCTCCACACCCCCATGTACTTCTTCT
TGTCGAACCTCTCTATCCTGGACATCCTCTTCACCTCAGTCATCTCTCCAAAAGTGTGGCC
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT
ACTTTTTCTTGGGCACAGTTGAGTTCCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC
35 ACCATCTGCTGCCCCCTGCGGTACACCACCATGAGACCTTCTGTCTGCATTGGGACCG
TTGTATTCTCTTGGGTGGGAGGCTTCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG
CTGCCCTTCTGTGGCTCCAATATCATTAACCACTTCTTCTGTGACAGTGACCCCTTGTGGC
CCTGGCCTGTGCAGACACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC
ATCCTCTGCTGCATAGTCCTCGTGGCCTATTCCTATACGTACATCATCTTGACCATAGTGCG
40 CATTCCTTCTGCAAGTGGAAGGAAGAAGGCCTTTAATACCTGTGCTTCCACCTGACCATA
GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCAGAAAGAATATCT
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCCTCAACCCCTTT
ATATATACTCTGAGGAATGACACAGTGACAGGGAGTCCCTCAGGGATGTGTGGGTGAGGGTT
CGAGGAGTTTTTGAAGAAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCTCCAACAAA
45 GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT
AG (SEQ ID NO: 156)

AOLFR85 sequences:

50 MGAKNNVTEFVFLFGLFESREMQHTCFVVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL
SFADICYPSTTIKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY
TAIMDCRKCGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV
GLIVVANSGMISLASFFILIISYVILLNLRQSSEDRRKAVSTCGSHVITVLLVLMPPMFMYIRPS
TTLAADKLLILFNIVMPPLNPLIYTLRNNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTATTTGGCCTTTTTGAGAGCAGAGAGA
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTCATGTGCTCACTGTCTGCGGGAACCTT

CTGGTCATCATCACCATCAATGCTAGAAAGACCCTGAAGTCTCCCATGTATTTCTTCCTGA
GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC
ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCA
CTTCTTTGGTGGCACTGAGATCTTCCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC
5 ATCTGTAGGCCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG
GGGCCTCCTGGTTAGCTGGCTTCCTGCATTCCATCCTGCAGACCCTCCTCACGGTTCAGCTG
CCTTTTGTGGGCCCAATGAGATAGACAACCTTCTTCTGTGATGTTTCATCCCCTGCTCAAGTT
GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT
Ttagcatccttttttatccttatcatttcttatgttatcatcttactgaacctaaagaagcca
10 gtcattctgaggaccggcgtaaggctgtctccacatgtggctcacacgtaatactgtcctt
ttggttctcatgccccccatgttcattgtacattcgtccctccaccacctggctgctgacaa
acttatcatcctctttaacattgtgatgccacctttgctgaacctttgatctataactaa
ggaacaacgatgtgaaaaatgccatgaggaagctgtttaggggtcaagaggagcttagggg
agaagtga (SEQ ID NO: 158)

15

AOLFR86 sequences:

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFFVFLLIYVTV
GNMLIVVITSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECCMAQLFGAHF
LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC
20 GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC
KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR
KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCTATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT
25 CTCAGTGACCTTGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGG
CTCTACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGCTGATCTATGTGG
TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC
CCCTGTGATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC
TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG
30 GCTCAGCTCTTTGGAGCTCATTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG
CTTATGACCGCTATGTGGCCATCTGTAAGCCCTGCACAATACTACCATCATGACCAAGCA
TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGCTTCTGCTTCTTCTTCTTCTG
CTCCTCCTGGTCTTTTGGTTGCCCTTCTGTGGGCCCAATGTGATCAATCACTTTGCCTGTGA
CTTGTACCTTTTGTGGAAGTTGCCTGCACCAATACGTATGTCAATTGGTCTGCTGGTGGTT
35 GCCAACAGTGGTTTAATCTGCCTGTTGAACCTCCTCATGCTGGCTGCCTCCTACATTGTCAT
CCTGTACTCCTTGAGGTCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA
GCCCACTTCATTGTTGTTGCCTTGTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATTT
TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA
TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA
40 TGGTAA (SEQ ID NO: 160)

AOLFR87 sequences:

MNNAQLSLGFIDLGPSVLQKIILTKIILLFKMYVSNCPNCAIHRKINYPNTKLDFEQVNNITEFI
LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIIVVTITTSALDSPVYFFLSFFSFIDGCSSTMAP
45 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVMA YDCYVAICKPLYLITMNRQVCGL
LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLKLSCTDTHVFGLFVAANSGLM
CMLIFSILITSYVLILCSQRKALSTCAFHITVVVFFVPCILVYLRPMITFPIDKAVSVFYTVVTPM
LNPLIYTLRNTTEVKNAMKQLWSQIIWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC
AGAAAATAATCCTGACCAAAAATTATTTTATTGTTCAAAATGTATGTGTCAAATTGCAATCC
TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAATGGATTTCGAGCAAGTGAAC
AACATAACGGAATTCATCTTGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT
TTGCTGTGTTTACACTCATCTACTTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA
55 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGATTTTTTTCTGTCTTTCTTTCTTCTCAT
AGATGGCTGCTCCTCTTCTACCATGGCCCCAAAATGATATTTGACTTACTCACTGAAAAG

AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCT
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAATAGTCTGGCTGCCCTTCTGTGGCCC
 5 CAATGTCATTGACCATTTCATCTGTGACCTTTTCCCTCTGCTAAAACCTCTCCTGCACTGACA
 CTCACGTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTCTACCTGCGC
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA
 10 AACCTTTAATCTACACCCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

AOLFR88 sequences:

MWQKNQTSLADFILEGLFDDSLTHLFLSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ
 15 LSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH
 PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFAVVKLVC
 GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRDVTQCIQRLQLWLP
 RV (SEQ ID NO: 163)

20 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT
 CCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCT
 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT
 25 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGTCCTATGACCGCTAT
 GTTGCCATCTGTCTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA
 TGGCTGTCTATGTCTATGGTTGGGGGCATCCGTGAACTCCCTAATTCATGCGCATCTTGAT
 GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCAGCTGTTG
 30 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT
 CCTCCTCCTCCCCATCTCCTGATTTCTACATCCTATGTCTTTCATCCTTCAAAGTGTCTTCA
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCTCCCACCTCACGGTG
 GTTTCTCTTGTGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGGTCCCAGTGCATCT
 ATTGCAAGACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCACATTGAATTCTCTG
 35 ATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT
 GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:
 164)

AOLFR89 sequences:

40 MLDPSISSHTLYLHSLFPQGLRKGTMWQKNQTSLADFILEGLFDDSLTHLFLSLTMVVFLIAVS
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTIILKMATNYLSGKKSISFVGCATQHFLYL
 CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF
 PFCGPRKVYHFYCEFAVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK
 RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA
 45 KALRRVLRDVTQCIQRLQLWLP RV (SEQ ID NO: 165)

ATGCTGGACCCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG
 GCTCTTCGATGACTCCCTTACCCACCTTTTCTTTTCTCCTTGACCATGGTGGTCTTCCTTAT
 50 TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA
 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA
 ACCCAGCACTTCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGTC
 CTATGACCGCTATGTTGCCATCTGTCTATCCACTGCGCTATGCTGTGCTCATGAACAAGAAG
 55 GTGGGACTGATGATGGCTGTCTATGCTGTTGGGGGCATCCGTGAACTCCCTAATTCACA
 TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA

5 GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC
ATCAGCAGCATTCTCCTCCTCCTCCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTT
CAAAGTGTCAATTCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT
CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG
TCCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCCA
CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT
GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG
TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF
VLLGLSQNPVQEIWFVFLFVYIATVGGNMLIVVTLSSPALLVSPMYFFLGFLSFLDACFSSVI
TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS
15 FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 167)

20 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTGGATGTACCAACTTGTAA
TGAATATGATACCACAAATTGATCTGAAGCAAATTTTCCTTTGCTTAATTGCAGACTATA
CATGATCCCTGTTGGAGCTTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA
ACTGAGTTTGTCTCCTCGGACTTTACAGAATCCAAATGTTAGGAAATAGTATTTGTTG
TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCATTTCTC
AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCTGCTCTTCTGGA
TGCCTGCTTCTCATCTGTATCACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA
25 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA
TACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG
GGCCTCTTGCAATCCATGATACAAATTCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC
30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG
TTGCTTGTCTCCTATGTCTCATCTTGTCTCTCTGAGAACACACAGTTCTGAAGGCGCTG
GAAAGTCTCTCCACCTGTGGATCTCATGCTGTTGTGATTTTGTGTTTGTGTTTGTGTTTGTG
TATTTGTATATACACGACCTCCATCTGCTTTTTTCCCTTGACAAAATGGCGGCAATATTTTAT
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC
35 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA
AACTTTAA (SEQ ID NO: 168)

AOLFR91 sequences:

40 MGNWSTVTEITLIAFPALLEIRISLFFVLVVTYTLTATGNITIISLIWIDHRLQTPMYFFLSNLSFL
DILYTTVITPKLLACLLGEEKTISFAGCMQTYFYFFLGTVFILLAVMSFDRYMAICDPLHYTVI
MNSRACLLLVLCWVGAFSLVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL
SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD
YDKVA AVLITVVTPLNPFYSLRNEKVQEVLRVTRNIMTLIQRKT (SEQ ID NO: 169)

45 ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA
TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT
CACCATCATCTCCCTGATATGGATTGATCATCGCTGCAAACTCCAATGTACTTCTTCCTCA
GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC
CTCCTAGGAGAAGAGAAAACCATATCTTTTGTGTTGATGATCCAAACATATTTCTACT
50 TCTTTCTGGGGACGGTGGAGTTTATCCTCTTGGCGGTGATGTCTTTGACCGCTACATGGC
TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT
CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTGTTTCCAACCATTGTAGTGACAAGGC
TACCTTACTGTAGGAAAGAAATTAATCATTCTTCTGTGACATTGCCCTCTTCTTCAGGTG
GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTATCCT
55 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC
CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCATCACTGTTGTCTCC

ATTGCCACGCGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT
ATGACAAGGTGGCCGCTGTCCTCATCAGTGGTGACCCCTCTCCTGAACCTTTTATCTA
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGACAGTGAACAGAATCATGAC
CTTGATACAAAGGAAACTTGA (SEQ ID NO: 170)

5

AOLFR92 sequences:

MRNGTVITEFILLGFPVIQGLQTPLFIAIFLTYILTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE
IWYTTTTVIPKLLGTFVVARVICMSCLLQAFFHFFVGTTEFLILTIMSFDRLTICNPLHPTIM
TSKLCLQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA
TILVIPGSLLFNMISYIYILSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

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ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC
TACAAACACCTCTCTTTATTGCAATCTTCTCACCTACATATTAACCTTGCAAGGCAATGGG
CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATTCCAATGTACTTCTTCCTTTG
TAACTTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAACTGCTAGGAACC
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGCAGGCCTTCTTCCACT
TCTTCGTGGGCACCCAGGTTCTTGATCCTCATCTATCATGTCTTTTGACCGCTACCTCACC
ATCTGCAATCCCCCTTACCACCCCATCATGACCAGCAAACCTCTGCCTGCAGCTGGCCC
TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTTGTGACACGATGCTGCTCATCCAGTT
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTTGA
GCCGCTGCATAGACACCAGCATTTTGAACCTCCTGGGCGTCATAGCAACCATCCTTGTA
TCCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA
ATTCCTTCAGCCACTGGCCACCAAAAGACTTTCTCTACCTGTGCCTCGCACCTGACAGTTGT
CTCCCTGCTCTACGGGGCTGTTCTGTTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

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AOLFR93 sequences:

MLMNYSSATEFYLLGFPGSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGH
L SALEILVTTHVPVMLWGLLLPGMQTIYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN
NTLTFEFILFLMAVFVLFGLIPTIVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCLFLY
VKPKQTQAADYNWVVSMLVSVVTPFLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID
NO: 173)

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ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA
ACTACATCATATCCTTTTGTCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA
CAGTCATCATCATGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTCTTCCTC
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG
GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG
TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG
TGGCTGTCTGTAAACCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT
GGTTCTTGTGTCTATGGGTGTTTGGGTTTCTTTTCAAATCTGGCCGGTCTATGTCATGTTT
AGCTTACTTACTGCAAAATCAAATGTGGTGAACAATTTTTTTGTGACCGAGGGCAATTGCT
CAAATACTCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTG
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTCTC
AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACCTG
TGTTGTGATTGGCTACGGCAGCTGCTTGTCTTCTACGTGAAACCCAAGCAAACGCAGGCA
GCTGATTACAATTGGGTAGTTTCCCTGATGGTTTCAGTAGTAACCTCTTTCCTCAATCCTTT
CATCTTACCCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC
TGTCAACTATTAGGAATTAG (SEQ ID NO: 174)

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AOLFR94 sequences:

METWVNQSYTDGFFLLGIFSHSTADLVLFSSVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF
LSQLSLMDLMLVCTNPVKMAANFLSGRKSISFVGGCIQIGLVCLVGSEGLLLGLMAYDRYVA
ISHPLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFCEMLSLLKLAC
5 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAVTLFYG
AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH
(SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC
10 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT
GGGAATGTCTCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCCATGTACTT
CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG
GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCCTTTGTGGGCTGTGGCATACAAATG
GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGCTGGGACTCATGGCTTATGACCG
15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC
AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT
AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC
TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGCTGTG
TCTTCATGCTTCTCTTCCCATTCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT
20 GTGCTGCAAATGCACTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCCTCCCACC
TGACAGCTGTCAACCCTCTTCTATGGGGCAGCCATGTTTCATCTACCTGAGGCCTAGGCACTA
CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCCTTACTCCCATGCTC
AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG
GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

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AOLFR95 sequences:

MLGSKPRVHLIYLPASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL
GNVGMMTIIMTDPRLNTPMYFFLGNLFSIDLFYSSVIEPKAMINFWSENKSISFAGCVAQLFLFA
LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRLCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS
30 RAVDHFYCDRPLQLRLSCSDLFIHRMISFSLSCIILPTIIVIVSYMYIVSTVLKIHSTEGHKKAFST
CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE
KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC
35 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCCAGG
CTTCAGGGTACGCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTGTGTTTATGCCA
TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC
ACCAATGTATTTTTCTAGGCAATCTCTCCTTCATTGATCTTTTCTATTCTGTTATTGA
ACCCAGGCTATGATCAACTTCTGCTGTAACAAAGTCTATCTCCTTGCAGGCTGTGTG
40 GCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC
TTATGACCGCTTTATTGCCATCTGCAACCCTCTGCTCTACTCTGTTCAAATGTCCACACGTC
TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTTGTGGCTGCATTAGCTCAGTTATTCAGACT
AGCATGACATTTACTTTATCTTTTTGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC
TCGCCCCTTCAGAGACTGTCTTGTCTGATCTCTTTATCCATAGAATGATATCTTTTTCT
45 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG
TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT
CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTTTTTATGTATCTCACTCCTGAC
AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA
ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAATTTCTAGA
50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

AOLFR96 sequences:

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLGNFLIVTVTSVDLALQTPMYFFLQN
LSLLEVCFVLVMVPKMLVDLVSPRKHSFVGGCTQMYFFFFFFGSSECFLLSMMAAYDRFVAICNP
55 LHYSVIMNRSCLWMAIGSWMSGVPVSMQLTAWMMALPFCGPNAVDFHFCGPPVLKLVTV
DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL

TYLRPKSNQSPESKKLVSLSYTVITPMLNPIIYGLRNNEVKGAVKRTITQKVLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC
CCGAGATGCAAGTTTCCCTCTTTATTTTTTTCCTGGCCATTTATACAGTCACTTTGTTGGGC
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT
TCTTCAAAATCTGTCACTTCTTGAAGTATGTTTCACCTTGGTTATGGTGCCAAAAATGCTTG
TAGATCTAGTGTCCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT
CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTTGT
10 GGCCATCTGTAACCCTCTCCATTATTCAGTCATAATGAACAGGTCCCTATGCTTGTGGATG
GCCATAGGCTCTTGGATGTCCGGTGTTCCTGTGTCTATGCTACAGACAGCTTGGATGATGG
CCCTTCTTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCCAGTGTTA
AACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT
TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG
15 AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT
GGTGTCCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACCAGTCC
CCTGAGAGCAAGAAGCTAGTGTCAATTGTCTACACTGTCATCACACCTATGCTAAACCCCA
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAAA
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

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AOLFR97 sequences:

MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVMVPSFSIAEHWRRMKGANLSQGMFEL
LGLTTDPQLQRLLFVFLGMYTATLLGNLVMFLLIHVSATLHTPMYSLKLSFLDFCYSSTVV
PQTLVNFLAKRKVISYFGCMTQMFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPEVC
25 ASLVGSYSAGFLNSLIHTGCIFSLKFCGAHVVTHFFCDGPPLSLSCVDTSLCEILLFIFAGFNLLS
CTLTILISYFLILNTILKMSSAQGRFKAFTSCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRTVA
VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

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ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT
CCTTAGGCAGAATTAAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT
GGAGTTTGAGCTCTTGGGCCTCACCACTGACCCCCAGCTCCAGAGGCTGCTCTTCGTGGTG
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTCTCTCTGATCCATG
TGAGTGCCACCCTGCACACACCCATGTACTCCCTCCTGAAGAGCCTCTCCTTCTTGGATTTC
35 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTCTTGGCCAAGAGGAAAGTGA
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCAGTGAGTGC
TATCTCATCGCTGCCATGGCCTATGACCGCTATGCCGCTATTTGTAACCCCCCTGCTCTACTC
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATGTGGGCTCCTACAGTGCAGGATTC
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTGCT
40 CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCCTTGTCTTGTGTAGACACCTCACTGT
GTGAGATCCTGCTCTTCATTTTTGCTGGTTTCAACCTTTTGAGCTGCACCCTCACCATCTTG
ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAATGAGCTCGGCCCAGGGCAGGTTTA
AGGCATTTTCCACCTGTGCATCCCACCTCACTGCCATCTGCCTCTTCTTTGGCACAACACTT
TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA
45 TCTACACAGTGGTGATCCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

AOLFR98 sequences:

MRGFNKTTVVTFQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEFI
50 LSFSESCYTFVIIPQLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR
YTLIINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE
LALFSLSILVIMVPFLILISYGFIVNTILKIPSAEGKKAFTVCASHLTVFVHYGCASIIYLRPKSK
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

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ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTCTCCAGCC
TGGGGGAGCTCCAGCTGCTGCTTTTTGTGTCATCTTCTCTCCTATACTTGACAATCCTGGTG

GCCAATGTGACCATCATGGCCGTTATTCGCTTCAGCTGGACTCTCCACACTCCCATGTATG
 GCTTTCTATTTCATCCTTTTCATTTTCTGAGTCCTGCTACACTTTTGTTCATCATCCCTCAGCTGC
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT
 CTTTTTCCTTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT
 5 ATGTAGCAATTTGTACCCTCTGAGGTACACACTCATCATAAACAAGGCTGGGGTTGGA
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATTT
 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC
 CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT
 10 CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT
 GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT
 CTTGTCTACAGTCTGAGGAACAAAGAGGTAACAACTGCATTGAAAAGAGTTCTTGGAATG
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

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AOLFR99 sequences:

MERVNETVVREVIFLGFSSRLRLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC
 SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSLFLGCSHSFLLAVMGYDRYIAICNPLRYSV
 LMGHGVCMGLVAAACACGFTVAQIITSLVFHLPFYSSNQLHFFCDIAPVLKLASHHNHFSQIV
 20 IFMLCTLVLAIPLLLLVSYVHILSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFIYLRPQSNY
 SSSQDALISVSYTHITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG
 CCAGGCTGCAGCAGCTGCTCTTGTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC
 25 AATGCAATCATCATTTCCACCATTGTCCTGGACAGGGCCCTTCATATCCCCATGTACTTCTT
 CCTTGCCATCCTCTCTTGTCTCTGAGATTTGCTACACCTTCATCATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCAGAAGAAGACCATTTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCCTCTTCCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT
 AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA
 30 GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCATCCTTGGTATTTC
 CCTGCCTTTTATTCCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGCTCA
 AGCTGGCATCTCACCATAACCACTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC
 CTGGCTATCCCCTTATTGTTGATCTTGGTGTCTATGTTACATCCTCTCTGCCATACTTCA
 GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCATTATTG
 35 TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAACCTACTCCTCA
 AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA
 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT
 TTCCCTGTTGTAA (SEQ ID NO: 186)

40 **AOLFR101 sequences:**

MDTGNWSQVAEFILGFPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI
 LSFSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL
 HYPTLMTPTLCAEIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDFPVLSLACTDTSINV
 45 LVDFVINSCKILATFLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVLIFYGSILSMYVQLK
 KSYSLDYDQALAVVYSVLTPLNPFYSLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC
 AGGGTGTCCAGATTTATCTCTTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA
 AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT
 50 TTGTCAGCATTCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG
 GCAAACCTTGCTCAGTGAGAAAAAGACCATTTCACTCTCTGGGTGTCTCCTGCAGATCTATT
 TCTTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA
 TTAGCCATCTGCCGGCCCCCTCCACTACCAACCCTCATGACCCCAACACTTTGTGCAGAG
 ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTTGATTT
 55 CACGCCTCCCATTCTGTGGCCCCAATCGCATTACAGCACGTCTTTTGTGACTTCCCTCCTGTG
 CTGAGTTTGGCTTGCATGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG

AOLFR105 sequences:

MQGLNHTSVSEFILVGFSAPHLQLMLFLLFLLMYLFTLLGNLLIMATVWSERSLHMPMYLFLC
ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL
RYNVLMSLRGCTCRVGCWAGGLVMGMVVTSIAIFHLAFCGHKEIHHFFCHVPPLKLACGDD
5 VLVVAKGVGLVCITALLGCFLILLISYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS
VIYLPKPKGPQSPEGDTLMGITYTVLTPFLSPIHSLRNKELKVMKKTCFTKLPQNC (SEQ ID
NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC
10 CCACCTCCAGTCGATGCTCTTCTGCTGTTCCTGCTGATGTACCTGTTACGCTGCTGGGCA
ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT
CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGGCCATCATCCCGCGCATGCTG
GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCCTGGCCTGTGCCAGTCAGATGTTCTT
CTCCTTCAGCTTCGGCTTCACCCACTCCTTCCTGCTCACTGTCATGGGCTACGACCGCTACG
15 TGGCCATCTGCCACCCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG
GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC
CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTCTGCCACGTGCCACCTCTGTT
GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT
CACGGCCCTGCTGGGCTGTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA
20 TCTTGAAGATCCCTTCTGCTGAAGGTCGGAACAAGGCCCTTCTCCACCTGTGCCTCTCACCT
CACTGTGGTGGTCGTGCACTATGGCTTTGCCTCCGTCATTTACCTGAAGCCCAAAGGTCCC
CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCCTCACACCCTTCCTCA
GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTCGCCATGAAGAAGACTTGCTT
CACCAAACCTCTTCCACAGAAGTGTGA (SEQ ID NO: 194)

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AOLFR106 sequences:

METANYTKVTEFVLTLGLSQTPEVQLVLFVIFLSFYLFILPGNIIICTISLDPHLTSPMYFLLANLA
FLDIWYSSITAPEMLIDFFVERKIIISFDGCIQLFFLHFAGASEMFLLTVMADFLYTAICRPLHYA
TIMNQRLCCILVALSWRGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
30 ICSSGLISVVCIALLLMSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVLTMFGPSIYIYARPD
SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
CAGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
35 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCTT
GTTGGCTAATCTGGCCTTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA
CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG
40 GTGGCTCTCTCCTGGAGGGGGGCTTCATTCACTCTATCATAACAGGTGGCTCTCATTGTTT
GACTTCTCTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT
CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG
ATCTCTGTGGTGTGTTGATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTTGTTCAA
GAAACTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCACATT
45 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCGTT
TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCCTTTACGTAATCCCATT
TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTACCAAATATA
TTTTGTGTAAGAGAAGTGA (SEQ ID NO: 196)

AOLFR107 sequences:

MELWNFTLGSFILVGILNDSGSPELLCATITILYLLALISNGLLLLLAITMEARLHMPMYLLLGQ
LSLMDLLFTSVVTPKALADFLRRENTISFGGICALQMFLALTMGGAEDLLAFMAYDRYVAICH
PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPCRAQEIRHLLCEIPHLLKVACAD
TSRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGA
55 ATFMVLPSSFHSTRQDNIIISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL
(SEQ ID NO: 197)

5 ATGGAGCTCTGGAACCTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGCTCCACATGCCCATGTACCTC
 10 CTGCTTGGGCAGCTCTCTCATGGACCTCCTGTTACATCTGTTGTCACTCCCAAGGCCCT
 TGCGGACTTTCTGCGCAGAGAAAAACCATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT
 CTGGCACTGACAATGGGTGGTGTGCTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT
 ATGTGGCCATTTGTCATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT
 CATGGTGGCCACGTCCTGGATCCTGGCATCCCTAAGTGGCCTAATATATACCGTGTATACC
 15 ATGCACTATCCCTTCTGCAGGGCCCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACT
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT
 GACCTTCTGATTCCCTCTCTTGTGCTATACTGGCCTCCTATACACAAATCTACTCACTG
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCCACCT
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGCCCAGTTCCTTCC
 20 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACCTCCAGCCCTGAA
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTATGCGGGCCTTGAGGAGGGTCTGGG
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

AOLFR108 sequences:

20 MCSFFLCQTKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIYLLTVLGNQLIILIFLD
 SRLHTPMYFFLRNLSFADLCFSTSIVPQVLVHFLVKRKTISFYGCMTQIIVFLLVGCTECALLAV
 MSYDRYVAVCKPLYYSTIMTQRVCLWLSFRSWASGALVSLVDTSFTFHLPHYWGQNIINHYFCE
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNIISTVIQMQSGEGRKAFSTCGSHLI
 25 VVVLFGSGIFTYMRPNSKTTKELDKMISVFYTAVTPMLNPIIYSLRNKDVKGALRKLVRKRC
 FSHRQ (SEQ ID NO: 199)

30 ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCAGAT
 CCTGCTATTTATCCTTTTCTCATATTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA
 TCATTCTCATCTTCTGATTCTCGCCTTCACTCCCATGTATTTTTTCTTAGAAATCTCT
 CCTTTGCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTGTTGTTCACTTCTTGGTA
 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAAATTGTCTTTCTTCTGGTTG
 GGTGTACAGAGTGTGCGCTGCTGGCAGTATGTCCTATGACCGGTATGTGGCTGTCTGCAA
 35 GCCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAAGTCTCT
 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC
 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT
 40 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGTCTCTT
 CTATGGGTCAGGAATATTCACCTACATGCGACCAAACCTCCAAGACTACAAAAGAACTGGA
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT
 CATAGGCAGTGA (SEQ ID NO: 200)

AOLFR109 sequences:

45 MLRNGSIVTEFILVGFAQSSTSTRALLFALFLALYSLTMAMNGLIIFITSWTDPKLNSPMYFFLG
 HLSLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGAECILLAFMAYDRYVAICY
 PLNYVPIISQKVCVRLVGTAWFFGLINGIFLEYISFREPFRRDNHIESFFCEAPIVIGLSCGDPQFSL
 50 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN
 PHSTHGPDKDKPFSLLYTIITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:
 201)

55 ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTTCAAGCAGAGCTCCA
 CTTCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG
 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT
 TCTTCCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACCCTACCATCCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT
 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCTATGACCGT
 TATGTTGCTATCTGCTACCCACTTAACATATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA
 GGCTTGTGGGAACTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTT
 5 ATTCCGAGAGCCCTTCCGCAGAGACAACCACATAGAAAGCTTCTTCTGTGAGGCCCCCATA
 GTGATTGGCCTCTCTTGTGGGGACCCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA
 TCGTGGTAATTCTCAGCCCCATGGTGCTCACTGTCACTTCCTATGTGCACATCCTGGCCACC
 ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTCTACTTGTGCCTCTCACC
 TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA
 10 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG
 GAAGAACCAGGCTGGCCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

AOLFR110 sequences:

15 MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLIILPGNFLIIFTIRSDPGLTAPLYLFLGNLAFL
 DASYSFIVAPRMLVDLSEKKVISYRGCTQLFFLHFLGGEGLLLVVMAFDRIAICRPLHCST
 VMNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVRQVIKLACTDMFVVEL
 LMVFNGLMTLLCFLGLASYAVILCHVRRASEGKNKAMSTCTTRVIIIIMFGPAIFIYMCPP
 20 RALPADKMVSLFHTVIFPLMNPMIYTLRNQEVKTSMKRLLSRHVVCQVDFIIRN (SEQ ID NO: 203)

ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA
 AATTTTCTCATTATTTTACCATAAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT
 25 TCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTATTGTGGCTCCCAGGATGTTGG
 TGGACTTCCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT
 CTTGCACTTCCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA
 TGATGTTGGCTCTGTGGCTTGGGGTTTTGTCCACTCCATTATCCAGGTGGTCCCTCATCCTC
 30 CGCTTGCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTGTGATGTCCGACAGGTCA
 TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT
 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTATGCAGTCATCCTCTGCCATGTTT
 GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCTATTA
 TTATACTTCTTATGTTTGGACCTGCTATCTTATCTACATGTGCCCTTTCAGGGCCTTACCA
 35 GCTGACAAGATGGTTTTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA
 TACCCTTCGCAACCAGGAAGTGAAGAACTTCCATGAAGAGGTTATTGAGTCGACATGTAGTC
 TGTCAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

AOLFR111 sequences:

40 MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCILHSILFLLIYLCALM
 GNVLIIMITTLDDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANSIHNNSISFLGCVSQVFLLLSS
 ASAEALLLVMSFDRYTAICHPLHYDVIMDRSTCVQRATVSWLYGGGLIAMHTAGTFSLSYCG
 SNMVHQFFCDIPQLLAISCENLIREIALILINVLDFFCFIVIIITYVHVSTVKIPSTEGQSKAY
 45 SICLPHLLVVLFLSTGFIAYLKPASESPSILDAVISVFYTMPLPPTFNPIIYSLRNKAIKVALGMLIKG
 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT
 TTTCTGCGAGATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA
 TGGGGTTTTCTACCAATAAAAAATATGTGCATTTTGCATTTCGATTCTCTTCTTGTGATTTAT
 50 TTGTGTGCCCTGATGGGGAATGTCCTCATTATCATGATCACAACCTTGGACCATCATCTCC
 ACACCCCCGTGATTTCTTCTTGAAGAATCTATCTTTCTTGGATCTCTGCCTTATTTAGTC
 ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCATTTCATTCTTGGCTG
 TGTTCCTCCAGGTCTTTTTGTGCTTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA
 TGTCTTTGACCGCTATACTGCTATATGTACCCCTCTGCACTATGATGTCATCATGGACAGG
 55 AGCACCTGTGTCCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTTCTTCTGT

5 GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAAATTGCACTCA
TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC
GTCTTCTCTACAGTCAAGAAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT
GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCAATTGCTTATCTGAAGCCA
GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCCC
AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG
TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

AOLFR113 sequences:

10 MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP
SVVTCSSSQSSDWMQLCTHLCTTSLVFFPSWSCGIQLPLSLRCLIFSRRKPFLQDASFRPTSS
TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF
CAYNEIQHIFCDFPPLLSLACKDTSANILVDFAINAFILITFFFIMISYARIIGAVLKIKTASGRKK
15 AFSTCASHLAVVLIFFGSIIFMYVRLKKSYSLTLDRTLAIVYSVLTMPMVNPIIYSLRNKEIKAIKR
TIFQKGDKASLAHL (SEQ ID NO: 207)

20 ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA
AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC
CTTCCTCCTTGTTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA
GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA
TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA
TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG
CTTTAGTGCTTGTTCCTCACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG
25 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA
GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT
AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT
GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA
GCAGTCTCTACAGTCTGATTGGTTCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT
GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA
30 AGCATTAAGCACATGTGGCTCCCATGTGGGGTTATGGCTTTGTACTATCTACCTGGGATG
GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGATGTCCTTGACACACCAAGTCCTGC
TAGCTGACCTGTACGTGATCATCCCAGCCACCTAAATCCCATCATCTATGGCATGAGGAC
CAAACAAGTGCAGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC
CTGGGTTCATGA (SEQ ID NO: 208)

35

AOLFR114 sequences:

40 MERINHTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTITGNLLIILAIRFNPHLQTPMYFFLSFLS
LTDICFTTSVHPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDYVAVCDPF
HYVTMTSHHVCVLLVAFSCSPHLLSLHLLNRLTFCDNSVIHHFLCDLSPVLKLSCSSIFVN
EIVQMTSEAPIVLVTRFLCIAFSYIRILTVLTKIPSTSGKRKAFTSCGFYLTVTLFYGSIFCVYLQP
PSTYAVKDHVATIVYTVLSSMLNPFYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

45 ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC
GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC
AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCATCTTCAGACCCCTATGTATT
TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCCAAGATG
CTGATGAACTTCCTGTCAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT
ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG
CTATGTGGCCGTCTGTGACCCTTTCCACTATGTCACCACCATGAGCCACCACCACTGTGTCC
50 TGCTGGTGGCCTTCTCCTGCTCATTTCTCCTCACCTCCACTCACTCCTGCACACACTTCTGCTG
AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCACCTTCTCTGTGACCTCAGCCCTGT
GCTGAAATTGTCCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT
ATTGTTTTGGTGAAGTCTTTCTCTGCATTGCTTTCTTATATACGAATCCTCACTACAGT
TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAAGCCTTCTCCACCTGTGGTTTTTACCTCA
55 CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGTCTATTTACAGCCCCCATCCACCTAC
GCTGTCAAGGACCACGTGGCAACAATTGTTTACACAGTTTTGTTCATCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA
GATCCTAG (SEQ ID NO: 210)

AOLFR115 sequences:

5 MEGFYLRSSHQLQGMGKPGRVNQTTVSDFLLLGLSEWPPEEQPLLFGIFLGMYLVTMVGNNLLII
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHTLLLTRVAFCAQK
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPPLLIVFSYVRIFWAVFVISSPGGRWKA
FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIPTLNPFIYSLNRNRMKEALG
10 KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC
15 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA
CCTGTCATTAAGTATGTCCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAAACATTC
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGTCTTGACACAGCTATATTTCTCCTTATG
TTTGGTGGCCTTGACAACTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT
GCCAACCCTCCATTACAGCACATCTATGAGTCCCAGCTCTGTGCACTAATGCTGGGTGT
20 GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT
TTCTGTGCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC
CTGCTCAGATACCCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCACT
GTTCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTCATCTC
ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTTCTCATCTCACGGTGGTTCTG
25 CTCTTCTATGGGTCTCTTATGGGTGTGTATTTACTTCTCCATCAACTTACTCTACAGAGAG
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATTCACGCTAAACCCATTCATTTAT
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTGAGTGGAAAAACA
TTCTTTTTATGA (SEQ ID NO: 212)

AOLFR116 sequences:

30 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLQSPMYFLLAN
LSIINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH
YLTIMNPQRCILFLVISWIIHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV
TANSGFISLASFLILIIISYIFILVTVQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPPTSHLD
35 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCCTGGGACTCTCTGACTCGC
GGAAGATCCAGCTCCTCCTCTTCTCTTTTCTCAGTGTTCTATGTATCAAGCCTGATGGGA
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCTCGTTTACAGTCCCCCATGTACTTCCT
40 GCTGGCCAAACCTTTCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT
ATGACCTTTTCAGGAAGCACAAGACCATCTCTTTTGGGGGCTGTGTAGTTCAGATCTTCTT
TATCCATGCAGTTGGGGGAACCTGAGATGGTGCTGCTCATAGCCATGGCTTTTGACCGATAT
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT
TTTTAGTCATTTCTGGATTATAGGTATTATTCACTCAGTGATTGAGTTGGCTTTTGTGTA
45 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTAT
CAAACTGGCTTGATAGACCTACACATTGGGATTGATGGTTACTGCCAATAGTGGATT
ATTTCTCTGGCTTCTTTTAAATTCTCATAATCTCTTACATCTTTATTTTGGTGACTGTTTCTCAG
AAAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTCAGCTCATGTCATTGTGG
TGGTTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTCCACATCACATCTTG
50 ATAAATCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTGAATCCAGTCATCTATACT
TTTAGAAATAAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC
AGTAAATCTTTTAA (SEQ ID NO: 214)

AOLFR117 sequences:

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLLAMTLGNSTEVTEFYLLGFGA
QHEFWCILFIVFLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSF

EEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI
MGSINASVQTGFTCSLSFCKSNSINHHFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS
YIYIMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215)

5

ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTTCTGGGTCCTTCTCTTGGTC
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC
TTCTGGGATTTGGTGCCAGCATGAGTTTTGGTGTATCCTCTTCATTGTATTCTTCTCATC
10 TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT
TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG
GCTGTGTGATAACAATTCTTAGTTTATGCAACATTTGCAACCAGTGACTGTTATCTCCTGGCT
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCTTCACTATACTGTAATCATGT
15 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC
TGTAACAAACAGGTTTACATGTTCACTGTCTTCTGCAAGTCCAATAGCATCAATCACTTTT
TCTGTGATGTTCCCCCTATTCTTGCTCTTTCATGCTCCAATGTTGACATCAACATCATGCTA
CTTGTTGTCTTTGTGGGATCTAAGTTGATATTCACTGGGTTGGTCGTCATCTTTTCTACAT
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA
20 ACATGTGCTTCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT
GCAGTCTCATTCTAATAATTCCCAGGAAAAATATGAAAGTGGCCTTTATATTTTATGGCACA
GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT
TAAAAGTGATAGGGAAGGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWSLPLALLYLSALAANTLILIIWQNPSLQQ
PMYIFLGILCMVDMGLATTIIPKILAIFWFDKVISLPECFAQIYAIHFFVGMESGILLCMAFDY
VAICHPLRYPISIVTSSLILKATLFMVLNRGLFVTPVPVLAQRDYCSKNEIEHCLCSNLGVTSLA
CDDRRPNISICQLVLAWLGMGSDLSLIILSYILILYSVLRNLNSAEAAKALSTCSSHLTLILFFYTIV
30 VVISVTHLTEMKATLIPVLLNVLHNIIPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCCAGGTCTCTGAGTT
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCCTGGCA
35 CTACTGTATCTCTCAGCACTTGCTGCAAAACACCCTCATCCTCATCATCTGGCAGAACCC
TTCTTTACAGCAGCCCATGTATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTGG
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT
ACTCTGCATGGCTTTTGATAGATATGTGGCTATTTGTACCCTCTTCGCTATCCATCAATTG
40 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGCTGAGAAATGGCTTATTTGTC
ACTCCAGTGCCTGTGCTTGCAGCACAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT
TTGCCAGTTGGTTCTGGCATGGCTTGGGAATGGGGAGTGATCTAAGTCTTATTATACTGTCA
TATATTTTGATTCTGTACTCTGTACTTAGACTGAACCTCAGCTGAAGCTGCAGCCAAGGCC
45 TGAGCACTTGTAGTTCACATCTCACCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCTACTTAATGTGTTGC
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAAGAAGCTTAG
GGCAGCCTTCCAAAAGGTGCTGTTTGCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:
218)

50

AOLFR119 sequences:

MPLFNSLCWFPTIHTVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP
MYFFFGHALSLIDLLTCTTLPNALCIFWFSLKEINFNACLAQMFFVHGFTGVESGVLMMLD
RYIAICYPLRYATTLTNPIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNIISHTYCDHMSVVKL
55 SCASIKVNVYGLMVALLIGVFDICISLSYTLILKAAISLSSSDARQKAFSTCTAHISAIITYVPA

FFTFFAHRFGGHTIPPSLHIIIVANLYLLLPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA
ATGTACATCATCTTCCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTATTATGAGGAGTC
CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG
CACCACCACTCTACCCAATGCACCTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA
10 ATGCTTGCTTGGCCAGATGTTCTTTGTTTCATGGGTTACAGGTGTGGAGTCTGGGGTGCT
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCTTTGCGTTATGCTACCACAC
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCCTGAGGGGTGTATTGCTGAT
GATTCTTTTCCCATTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCATA
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT
CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGTTGACATTTGTTGTATATCTTTGTCTT
15 ACATTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT
CAGCACTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT
TCTTTGCCACCGTTTTTGGGGACACAAATCCCCCTTCTCTTCACATCATTGTGGCTAAT
CTTTATCTTCTTCTTCCCCCAACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

20

AOLFR120 sequences:

125 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAHLVVGDLHRLRRPMYF
FLTHLSCLEIWTYSVTVPKMLAGFIGVDGKNISYAGCLSQLFIFTFLGATECFLLAAMAYDRY
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPIPIYLLSQLTFCGPNVIDHFSCDASPLLALS
25 CSDVTWKETVDFLVSLAVLLASSMVIASVGNIVWTLHIRSAAERWKAFTCAAHLTVVSLF
YGTLLFFMYVQTKVTSSINFNKVVSFVSVTPMLNPLIYSLRNKEVKGALGRVFSLNFWKQG
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTTCCTCACCATGTACCTGTTACCTTG
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT
ATTTCTTCTGACACACTTGCTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAAATATCTCTTATGCTGGTTGCCTAT
35 CCCAGCTCTTCATCTTCACCTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC
TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCTGGGGCAC
CTGCATCCGCTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCCTCACACCCATCTTGCCAATCT
ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTCTCTCTGTGATGCC
TCACCCTTGCTAGCCTTGTCGTGCTCAGATGTCACTTGGAAGGAGACTGTGGATTTCTCTGG
TGTCTCTGGCTGTGCTACTGGCTCCTCTATGGTCATTGCTGTGTCTATGGCAACATCGTC
40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG
GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCCAT
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTGAGTC
TTTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

45

AOLFR121 sequences:

125 MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFVLTVYILTLVANIIVTIICIDHHLHTPMYFFLSMLA
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFFVILATNNCFLLTAMGYDRYVAICRPLRY
TVIMSKGLCAQLVCGSFGLTMAVLHVTAMFNLPCGTVVDHFFCDIYPVMKLSCIDTTINEII
50 NYGVSSSFVIFVPIGLFISYVLVISSILQIASAEGRKKTFATCVSHLTVVIVHCGCASIAYLKPKSES
SIEKDLVLSVTYTIITPLNPVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTTAACCTGTCTACATTTTAACTCTGGTTGCT
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTTCTT
CCTAAGCATGCTGGCTAGTTCAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTTTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT
TTTTGTTATCTTGGCCACTAATAATTGCTTCCTGCTTACTGCAATGGGGTATGACCGCTATG
TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT
5 GGTGTGTGGGTCCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTT
AATTTGCCGTTCTGTGGCACAGTGGTAGACCACTTCTTTTGTGACATTTACCCAGTCATGA
AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAAGTTCATTTGT
GATTTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTCTCTCTTCCATCCTTC
AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCACCTCACTGT
10 GGTTATTGTCCACTGTGGCTGTGCCTCCATTGCCTACCTCAAGCCGAAGTCAGAAAGTTCA
ATAGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTTGCTGAACCCTG
TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA
ATATTTCTTAA (SEQ ID NO: 224)

AOLFR122 sequences:

15 MEWENQILVEFFLKGHVHPRELLFFVLIFIMYV VILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTSPSTLVSFLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN
EFLMLVATILFTLMPLLLIVISYSLIISILKHSSEGRSKAFSTCSAHLTVVIIIFYGTILFMYMKPKS
20 KETLNSDDLDATDKIISMIFYGVMTMPMNPLIYSLRNKDVKEAVKHLPNRRFFSK (SEQ ID NO:
225)

ATGGAATGGGAAAACCAAACCAATTCTGGTGAATTTTTTCTGAAGGGACATTCTGTTACCC
CAAGGCTTGAGTTACTCTTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCCTTCTGGGG
25 AATGGTACTCTCATTTTAATCAGCATCTTGGACCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCTTTTCTGGCTGTGCAAGTGCAGATGTTCTT
GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG
TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT
30 GGCTGTTGGGTCTGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA
CAATTGCCTTTCTGCAGGAAGAATGTCATCAATCATTCTCATGTGAAATTCTAGCTGTCAT
GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCTCTCATGCTTGTGGCCACAATATTG
TTCACATTGATGCCACTGCTCTTGATAGTTATCTTACTCATTAAATCATTTCAGCATCCT
CAAGATTCACCTCTGAGGGGAGAAAGCAAGCTTTCTCTACCTGCTCAGCCCATCTGACT
35 GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA
CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT
GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT
AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

AOLFR123 sequences:

40 MYRFTDFDVSNISIYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL
IMYMILLGNSLLIITILDSRLHTPMYFFLGNLSFLDICYTSSSIPPMLIIFMSERKSISFIGALQM
VVSLLGLSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLYVQMAAWSWIIGCLTSLLQTVLT
MMLPFCGNNVIDHITCEILALLKLVCSGITINVLIMTVTNIVSLVILLLLIFISYVFILSSILRINCAE
45 GRKKAFSTCSAHSIVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV
KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT
CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT
50 GACTGAATTTCTTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTTCTGTTCTGCT
TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC
TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT
CTGTTACACATCCTCATCCATTCTCCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA
TCTCCTTCATTGGCTGTGCTCTGCAGATGGTTGTGTCCCTTGGCTTGGGCTCCACTGAGTGT
55 GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT
CCATCATCATGAACGGAGTGCTGTATGTGCAAAATGGCTGCATGGTCTGGATCATAGGCTG
TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC

ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT
CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT
TCATCTCCTATGTGTTTATTCTCTCTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG
AAAGCCTTCTCTACCTGTTGAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT
5 TTTTATGTACATGAAACCAAGTCAAAGAACTAATACATCTGATGAGATTATTGGGCTG
TCTTATGGAGTGGTAAGCCCAATGTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG
TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ
ID NO: 228)

10 **AOLFR124 sequences:**

MNHSVVTEFIILGLTKKPELQGIIFLFLIVYLVAFLGNMLIIIAKIYNNLTHTPMYVFLTLAVV
DIICCTSIIPKMLGTMLTSENTISYAGCMSQLFLTWSLGAEMVLFTTMAYDRYVAICFPLHYST
VMNHHMCMVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLLALSCSPVRINEV
MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRAKAFSTCSSHLTVVTLYYSPVIYTYIRPASS
15 YTFERDKVVAALYTLVPTLNPMVYSFQNREMQAGIRKVFAFLKH (SEQ ID NO: 229)

ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC
AGGGAATTATCTCCTCTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC
ATCATCATTGCCAAAATCTATAACAACACCTTGACATACGCCCATGTATGTTTTCTTCTGAC
20 ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT
GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCAGCTCTTCTTGTTCACA
TGGTCTCTGGGAGCTGAGATGGTTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA
TTTGTTCCTCTTTCATTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC
ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA
25 CTTTCTGTGGGCCAAACACCATTGACCACTTCTTCTGTGAGATACCCCCATTGCTGGCTTTG
TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA
TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC
CGCACAGTAGAAGGCAAGAGGAAGGCCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG
ACCTTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA
30 AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCCACATTAAACCCGATGGTG
TACAGCTTCCAGAATAGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTCTGAAA
CACTAG (SEQ ID NO: 230)

AOLFR125 sequences:

MTNQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH
LSFLDLCLISATVPKSILNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICCPHLC
EAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSEHAI
ISVSVAIGVCYAFSCLVCIVVSIVYIFSAVLRISQRQRQSKAFSNCVPHLIVTVFLVTGAVAYL
KPGSDAPSILDLLVSFYSVAPPTLNPIYCLKNKDIKSALS KVLWNRSSGVMKDD (SEQ ID
40 NO: 231)

ATGACCAATCAGACACAGATGATGGAATTCTTGCTTGTGAGATTTACTGAGAATTGGGTGC
TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA
45 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCG
ACATTTGTCCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT
CTGTCGCCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTTGCAGCTCTTCTTGGTGGTA
CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCCTATGACCGCTATGCTGCCA
TCTGCTGCCCCCTACACTGTGAGGCTGTGATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC
TCTGTCCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG
50 AATTTTTATGGCTCTGATGAGCTACATCAGTTCTTCTGCGATGTCCCTGCCCTACTAAAGCT
CACTTGTTCTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA
TTTTCATGTTTAGTTTGCATTGTAGTTTCTATGTGTACATTTTCTCTGCTGTGTTAAGGAT
ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATTGTTGTC
ACTGTGTTTCTTGTAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT
55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA
GCAGTGGGGTAATGAAAAGATGACTAA (SEQ ID NO: 232)

AOLFR126 sequences:

5 MFLYLCFIFQRTCSEEMEEENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYLITIMGNLGLIVLIW
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSFRLTFCNSNIIQHFYCDII
PLLKISCTDSSINFLMVFI FAGSVQVFTIGTILISYTHLFTILEKKSIKIRKAVSTCGAHL LSVSLY
10 YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID
NO: 233)

ATGTTCCCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT
15 ACCGCTCTTCCTGGCATTCTTGTAATATATCTCATCACCATCATGGGGAATCTTGGTCTAA
TTGTTCTCATCTGGAAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA
GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG
CTAAGAGTAAGATGATATCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT
GTAACCACAGAATGTTTTCTCTTGGAACAATGGCAGATATGATCGCTATGTAGCCATTTGCA
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTCAGCTATTAGTCTTGCA
20 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTCATTCAGATTAACCTTCTG
TAATTCCAACATAATAACAACACTTTTACTGTGACATTATCCCATTGTTAAAGATTTCTGTGTA
CTGATTCTCTATTAACCTTTCTAATGGTTTTTATTTTCGCAGGTTCTGTTCAAGTTTTTACCA
TTGGAAC TATTCTTATATCTTATACAATTATCCTCTTTACAATCTTAGAAAAGAAGTCTATC
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT
GATGGAGTCTCTATTTTACACTGTCATAGTTCCTTTATTAAATCCCATGATCTACAGCCTGA
GAAACAAGCAAGTAATAGCTTCATTCACAAAAATGTTCAAAGCAATGTTTAG (SEQ ID
NO: 234)

AOLFR127 sequences:

30 MSNEDMEQDNNTLLTEFVLTGLTYQPEWKMPFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM
YFFLGSLAFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY
VAICKP LLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIFRLTFCNSNIIHHFYCDIIPLMISCTD
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHL LSVSLY YGPLIF
35 MYLRPASPQADDQDMIDS VFYTHIPLLNPIIYSLRNKQVIDSFTKMVKRNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATAACAACATTGCTGACAGAGTTTGTCTCACA
GGACTTACATATCAGCCAGAGTGGAAAATGCCCCTGTTCTTGGTGTCTTGGTGATCTATC
40 TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTTCAC
ATCCCCATGTACTTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT
AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC
ATGATTCAATTTTTTCTTTGCAATTTGGTGGAAC TACAGAATGTTTTCTCTTGGCAACAAT
GGCATATGATCGCTATGTAGCCATATGCAAACCTTTACTATATCCAGTGATTATGAACAAT
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCTCCATGCCTTAATTCA
45 TGAAGTCCTTATATTAGATTAACTTCTGCAATTCTAACATAATACATCATTTTTACTGTG
ATATTATACCACTGTTTATGATTTCTGTACTGACCCTTCTATTAATTTCTAATGGTTTTTA
TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTTCTACACATTTGCT
CTTTTCACAATCCTAAAAAAGAAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT
50 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTTATACAATCATAATTC
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAAACAAGTAATAGATTTCATTCACAAA
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

AOLFR128 sequences:

55 METQNLTVVTEFILLGLTQSQDAQLLVFVLVLI FYLIILPGNFLIIFTIKSDPGLTAPLYFFLG NLA
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVM AFDRIYAICRPLHY

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVEL
LMVSNSSLGSLLCFLGLLASYAVILCRIEHSSEKSKAISTCTTHIIIFLMFGPAIFIYTCPPQAFP
ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMFC (SEQ ID NO: 237)

5 ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC
AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCACAGGATGTTG
GTGGACTTCCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT
10 TCTTGCAATTTCTTGGAGCGGGAGAGATGTTCCCTCCTCGTTGTGATGGCCTTTGACCGCTAC
ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG
CACTTGCCCTTCTGTGGCCCAAACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG
15 CTCAGCCTCCTGTGCTTCTTGGGCTTCTGGCCTCCTATGCAGTCATCCTCTGTGCTATAAG
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT
ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGCCCCCTCCAGGCTTTCCAGC
TGACAAGGTAGTTTCTCTTTTCCATACTGTCATCTTTCCTTTGATGAACCCTGTTATTTATA
CGCTTCGCAACCAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG
20 CTGA (SEQ ID NO: 238)

AOLFR129 sequences:

MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLLFALFSVI
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT
25 QIFLLHLLGGVEMVLLVSMADFVVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF
AVNLPFCGPNVVDISIFCDLPLVTKLACIDIYFVQVVIVANSGLSFCIILLISYSLILITIKNHSPT
GQSKARSTLTAHITVVILFFGPCIFIYIWPFGNHSVDKFLAVFYTHITPILNPIIYTLRNKEMKISMK
KLWRAFVNSREDT (SEQ ID NO: 239)

30 ATGGCTCTTTATTTTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTTCTCTCTACAGG
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAAATCAATCTCAAGTGTC
AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTTTTGGCCTCT
TCTCGGTTATCTATGTGGTCACAGTTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTTAAAC
ACCCCTAACCTGAATACTCCCATGTATTTTCTCCTTGGTAATCTCTCTTTTGTAGATATGAC
35 CCTTGCTTCTTTTGCCACCCCTAAGGTGATTCTGAACTTGTTAAAAAAGCAGAAGGTAATT
TCTTTTGTGCTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGTTGAAATGGT
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCCTACACTACATG
ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC
TTCACTCAGGGTTTCAGATAACATTTGCTGTGAACTTGCCCTTTTGTGGTCCCAATGTGGTA
40 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCTGTATAGACATATATTTTGT
ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGTCTA
TCTCCTACAGTCTGATCCTCATAACCATAAAGAACCACTCTCCTACTGGGCAATCTAAAGC
CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTTCTTTTGGCCCATGCATCTTTA
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC
45 ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

AOLFR131 sequences:

MASTSNVTELIPTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS
50 LVEISYSSTIAPKFIIDLLAKIKTISLEGCLTQIFFHFFGVAEILLIVVMAYDCYVAICKPLHYMNI
ISRQLCHLLVAGSWLGGFCHSHIILVIIQLPFCGPNVIDHYFCDLQPLFLACTDTFMEGVIVLA
NSGLFSVFSFLILVSSYIVILVNLNRNHSAGRHKALSTCASHITVVILFFGPAIFLYMRPSSTFTED
KLAVAFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG
TGCAGAGTGATGCTTTGTGGTGTTTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA
GCTGCCTGTCCTTGGTGGAGATCAGTTATTCCTCCACTATCGCCCCTAAATTTCATCATAGAC
TTACTTGCCAAAGATTAAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA
CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC
5 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTCACCTTCTGGTGGC
TGGTTCCTGGCTGGGGGGCTTTTGTCACTCCATAAATTCAGATTCTCGTTATCATCCAATTGC
CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT
GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTTGGCCAACAGTGGATTATTCTCTG
TCTTCTCCTTCTCATCTTGGTGTCTCTTATATTGTCATTCTGGTCAACTTGAGGAACCAT
10 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT
TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCACTGAAGATAAA
CTTGTGGCTGTATTCTACACGGTCATCACCCCATGCTGAACCCCATCATTTACACACTCAG
GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA
GGGAGTGA (SEQ ID NO: 242)

15

AOLFR132 sequences:

MVATNNVTEIIFVGFSSQNWSEQRVISVMFLMYTAVVLGNGLIVVTILASKVLTSPMYFFLSYL
SFVEICYCSVMAPKLIFDSFIKRKVISLKGCLTQMPSLHFFGGTEAFLLMVMA YDRYVAICKPL
HYMAIMNQRMCGLLVRIAWGGGLLSVGGTFLIFQLPFCGPNIMDHYFCDVHPVLELACADT
20 FFISLLIITNGGSISVVSFFVLMASYLILHLRSHNLEGQHKALSTCASHVTVVDLFFIPCSLVYIR
PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

20

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCCAGAATTGGAGTG
AGCAGAGGGTCATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG
25 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA
GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCATGGCCCCAAGCTTATCTTTGAC
TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTTCCCTCC
ATTTCTTTGGTGGCACTGAGGCCTTTCTCCTGATGGTGTGTCCTATGACCGCTATGTGGC
CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG
30 AGGATAGCATGGGGCGGGGGCTGTGCACTTCTGTTGGGCAAACCTTCTGATTTTCCAGC
TCCCGTTCTGTGGCCCCAACATCATGACCACACTTCTGTGATGTGCCACCCAGTGCTGGA
GCTGGCCTGCGCAGACACCTTCTTATTAGCCTGCTGATCATACCAATGGCGGCTCCATC
TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCTGCACTTCTGAGAAG
CCACAACCTTGAGGGGGCAGCACAAAGGCCCTCTCCACCTGTGCCTCTCATGTACAGTTGTC
35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACACCTCCCTGCAGA
CAAGATAGTTGCTGTATTTTATACAGTGGTCACACCTCTCTTAAACCCTGTGATTTACTCCT
TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA
(SEQ ID NO: 244)

40

AOLFR133 sequences:

MTEFIFLVLPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRSLGSPMYFFLSYLSFMEICYS
SATAPKLISDLLAERKVISWWGCMAQLFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN
WQVCTVLVGIAWVGGMHSFAQILLIFHLLFCGPNVINHYFCDLVPLLKLACSDTFLIGLLIVAN
GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI
45 DKMVAVFYTVITAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

45

ATGACTGAATTCATTTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG
TGATATTTCTGTCTTGACACAGCAATTGTGCTGGGGAATTCCTCATTGTGCTCACTGTC
50 ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTTCTCAGCTACCTCTCCTTCATGGA
GATCTGCTACTCCTCCGCTACAGCCCCCAAACCTCATCTCAGATCTGCTGGCTGAAAGGAAA
GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA
GATTTTCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCTCAGC
TACACCACCATCATGAACTGGCAGGTGTGTAAGTGTGCTTGTAGGAATAGCATGGGTGGGA
GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTGTGGCCCCAA
55 TGTGATCAATCACTATTTCTGTGACCTAGTTCCCTTCTCAAACCTGCCTGCTCTGACACCT
TCCTCATTGGTCTGCTGATTGTTGCCAATGGAGGCACCTGTCTGTGATCAGTTTGGGGT

55

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG
TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTCTTTGGGCCCTG
CGTCTTCAACTCTCTGAGGCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT
ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG
5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID
NO: 246)

AOLFR134 sequences:

MTTILEVDNHTVTTRFILLGFPTRPAFQLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL
10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC
NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSCE
DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYSMT
LFTYARPKLMYAYNSNKVVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTIHCRGSGPQNGAFS
S (SEQ ID NO: 247)

15 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTTCATTCTTCTGG
GGTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCCTGGCAACCTATCTG
CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA
AGCCCCATGTACTTCTTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC
20 AGCCCCAAGATGCTTGTGACTTCTCCTCAGTCATGACAAGAGTATTTCTTCAATGGCTGCA
TGACTCAACTTTACTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG
GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC
AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTTCTGTGGACTCATGACTGCCATGATTAA
GATGGTTTTTATAGCACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTGTG
25 ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT
CTTCTTGGCCCTCATGGTCATTGCTATTCTCTTTGTGTTGTGGTGGCATCCTACGCTGCTA
TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG
TGCCTCCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTCACCTATGCCCCGTC
CCAACTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCAATTGTT
30 CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA
AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTCAGTAGTTAA (SEQ
ID NO: 248)

AOLFR135 sequences:

35 MIFPSHDSQAFTSVDMEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILIRT
DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL
AAMAYDRHAAICNPLLYSGTMSTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIIDHFFC
DAPPLVKMSCTNTRVYEKVLGVVGFVLSILAILISYVNILLAILRIHSASGRHKAFSTCASHL
ISVMLFYGSLLFMYSRPSSTYSLERDKVAALFYTVINPLLNPLIYSLRNKDIKEAFRKATQTIQPT
40 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT
GCACCATCCTGACTGAATTCATCTTGTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT
TCTATTTGGAGTGTCTTCTGATGCTCTATTGATAACCTTGTGAGGAAACATGACCTTGGTTA
45 TCTTAATCCGAAGTATTCCCACCTGCATACACCTATGTACTTTTTCATTGGCAATCTGTCT
TTTTTGGATTCTGGTATACCTCTGTGTAATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA
AGATAAGCGCATTTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTTCTGTGTTGTAGCCT
ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC
ATTGCTTTATTACAGGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCCTACA
50 TAGGAGGATTTTTGAATGCCATAGCCATACTGCCAATACATTCCGCCTGCATTTTGTGG
TAAAAATATCATTGACCACTTTTTCTGTGATGCACCACCATTGGTAAAAATGTCCTGTACA
AACACCAGGGTCTACGAAAAAGTCCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA
TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT
TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA
55 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCACCTACTCCCTAGAGAGGGACAAA
GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG

AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG
A (SEQ ID NO: 250)

AOLFR136 sequences:

5 MTMENYSMAAQFVLDGLTQQAELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL
SSLSFVDFCYSSVITPKMLVNFLGKKNTILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC
SPLLYNAIMSSWVCSLLVLAFFLGLSALHTHSAMMKLSFCKSHIINHFCVDLPLLNLSCSNT
HLNELLFIAGFNTLVPTLAVAVSYAFILYSILHIRSSEGRSKAFGTCSSHLMAVVIFFGSITFMY
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAAACACAGCAAG
CAGAGCTCCAGCTGCCCCCTCTCCTCCTGTTCTGGAATCTATGTGGTCACAGTAGTGGG
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTACTATT
TCCTCAGCAGCTTGTCCCTTCGTCGATTTCTGCTATTCTCTGTCACTTCCCAAAATGCTG
15 GTGAACCTCCTAGGAAAGAAGAATAACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC
TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTGACTCATACAAGTGCCATGATG
AAACTGTCCTTTTGGCAAATCCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCCTCT
20 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTATCATTGCGGGGTTTA
ACACCTTGGTGCCCACTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGAACATGCAGCTCTCATCTCATGG
CTGTGGTGATCTTCTTTGGGTCCATTACCTTCATGTATTTCAGCCCCCTTCAAGTAACTCC
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAGGAAGGTCTTAGTAGGAA
AATGA (SEQ ID NO: 252)

AOLFR137 sequences:

30 MSPENQSSVSEFLLGLPIRPEQQAFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
LALTDISFSSVTPKMLNMNQTHLAVFYKGCISQTYFFIFFADLDSFLITSMA YDRYVAICHPL
HYATIMTQSQCVM LVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL
NQLAIFTAALTAIMLPFLCILVSYGHIGVTILQIPSTKGICKALSTCGSHLSVVTIYYRTIIGLYFLP
PSSNTNDKNILASVIYTA VTPMLNPFIYSLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ
ID NO: 253)

35 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCTCCTCCTGCGGCTCCCCATCCGGC
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTGCGGCATGTACCTGACCACGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTACTTCT
TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG
40 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT
TTTTCATATTTTTGCTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT
GTGGCCATCTGTATCCTCTACATTATGCCACCATCATGACTCAGAGCCAGTGTGTATGC
TGGTGGCTGGGTCTGGGTATCGCTTGTGCGTGTGCTCTTTTGATACCCTCCTCCTGGCC
CAGCTTTCCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT
45 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA
GCCATTATGCTTCCATTCTGTGCATCCTGGTTTCTTATGGTCACATTGGGGTCACCATCCT
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGCCACTTGTGGATCCCACTCTCA
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCATCCAGCAACAC
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA
50 TTCATTTACAGTCTGAGAAATAAAGACATTAAGGGAGCCCTAAGAAAACCTTTGAGTAGG
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

AOLFR138 sequences:

55 MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS
FVDVWFSSNVTPKMLENLFSKKTISYADCLAQCFFIALVHVEIFILAAIAFDRTYVIGNPLLY
GSKMSRGVCIRLITFPYIYGFLTSLTATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY

TMLILAGINFTYSLTVIIISYLFILAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTGGGGCTAACGAGCCGTCGGGAAT
GGCAAGTTCTCTTCTTCATCGTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC
GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTCCTCA
GTCACCTTGTCATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTAGCACAGTGTTCCTTCTTCAT
10 TGCTCTTGTCCATGTGGAAATTTTTATTCTTGTGCGATTGCCTTTGATAGATACACAGTGA
TTGGAAATCCTTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTTCGACTGATTAC
TTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTGCCGGCATCAACTTC
ACATATTCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTCCACATGTGGGTCCCATCTGACAGCTGT
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCCACAGAGGAGTCTGTG
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT
GTAA (SEQ ID NO: 256)

20

AOLFR139 sequences:

MGFPGIHSWQHWLSLPLALLYLLALSANILILIIINKEAALHQPMYYFLGILAMADIGLATTIMP
KILAILWFNAKTISLLECFQMYAIHCFVAMESSTFVCMADRYVAICRPLRPSIITESFVFKAN
GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSRDDRRINSINQVLLAWTLMGS
25 DLGLIILSYALILYSVLKLSPEAASKALSTCTSHLILILFFYTVIIVISITRSTGMRVPLIPVLLNVL
HNVIPPALNPMVYALKNELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

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35

40

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT
GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG
AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT
CTGCATGGCTATTGATAGATATGTAGCCATTTGTGCGACCGCTACGATATCCATCAATCATC
ACTGAATCTTTTGTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA
TCTCAGTGCCTCTGTTGGCTGCCCAGAGGCATTACTGCTCCCAGAATCAAATTGAGCACTG
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATT
AACCAGGTCCTTTTGGCTTGGACACTCAAGTGAAGTGAACCTGGGTTTGATTATTTTATCAT
ATGCTCTAATACTTTACTCTGTCTGAAGCTGAAGCTCTCCAGAAGCTGCATCCAAGGCCTT
AAGTACCTGCACCTCCCACCTCATCTTAATCCTTTTCTTCTACACAGTGCATCATGTGCTTT
40 CCATTACTCGTAGTACAGGAATGAGAGTTCCCCCTATTCCAGTTCTACTTAATGTGCTACA
CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAACCTCAGG
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

AOLFR140 sequences:

45 MLTLNKTDLIPASFILNGVPGLEDQLWISFPFCSMYVVMVGNCGLLYLIHYEDALHKPMYY
FLAMLSFTDLVMSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMMLMALDRYV
AICYPLRYSTILNPVIAKVGATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG
NVKVNAIYGLMVALLIGGFILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF
FSFFSHRFGHEHIIPPSCHIIVANIYLLLPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ
50 ID NO: 259)

55

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCCAG
GACTGGAAGACACACAACTCTGGATTTCCCTTCCCATCTGCTCTATGTATGTTGTGGCTAT
GGTAGGGAATTGTGGACTCCTCTACCTCATTCACTATGAGGATGCCCTGCACAAACCCATG
TACTACTTCTTGGCCATGCTTTCCCTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTGATGAATGCCTTGTCCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG
 ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTCACCAATCCTGTAATT
 GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGATTACTCATTATTCCCTTTACTTTTCT
 5 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG
 TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG
 CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCTTTAATACCTGCACTGCCC
 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCCACCGCTTTG
 10 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA
 CCCACTATGAACCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCTATAA
 GGATCCTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

AOLFR141 sequences:

MSSTLGHNMESPNTDVPVFFLLGIPGLEQFHLWLSLPVCGLTATIVGNITILVVVATEPVL
 15 HKPVYFLCMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHFMMESTVLLAM
 AFDYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCFLIGRLNFCQSHVILHTYCEHMA
 VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC
 VILISYTPALFSFFTHRFGHHVPVHIHILLANVYLLPPALNPVVYGVKTKQIRKRVVRVFQSGQ
 GMGIKASE (SEQ ID NO: 261)

20 ATGTCCAGCACTCTTGGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG
 TCTTCTTCTCCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG
 TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATACTATTCTGGTTGTTGTTGCCACTG
 25 AACCAGTCTTGCACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT
 GCCTCTGTCTCCACAGTTCCCAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACT
 GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA
 CAATCCTCACTGACACCATCATTGCCCACATAGGGGTGGCAGCTGTAGTGCAGGGCTCCCT
 30 GCTCATGCTCCCATGTCCCTTCTTATTGGGCGTTTGAACCTCTGCCAAAGCCATGTGATCC
 TACACAGTACTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA
 ACCGTGTGTATGGGCTGACAGCTGCATGTTGGTCACTTGGGGTTGACTTGTTTTGCATTGG
 TCTCTCCTATGCCCTAAGTGCACAAGCTGTCTTCTGCCTCTCATCCCATGAAGCTCGGTCCA
 AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTTATACACCAGCCCTC
 35 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTCACATTCTTTTGGC
 CAATGTTTATCTGCTTTTGGCACCTGCTCTTAATCCTGTGGTATATGGAGTTAAGACCAAAC
 AGATCCGTAAGAGAGTTGTCAGGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT
 CTGAGTGA (SEQ ID NO: 262)

AOLFR143 sequences:

40 MLGLNGTPFPATLQLTGIPGIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPYYFL
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVQMFFIHTFSFMESGILLAMSLDRFVAICY
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFPFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI
 HVNNIYGLLVIIFTYGMDSTFILLSYALILRAMLVISQEQRLKALNTCMSHICAVLAFYVPIAVS
 45 MIHRFWKSAPPVVHVMMNSNVYLFVPPMLNPPIYSVKTKEIRKGILKFFHKSQA (SEQ ID NO:
 263)

50 ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAAACTCCAGCTGACAGGCATTCTCTG
 GGATACAAACAGGCCTCACCTGGGTTGCCCTGATTTTCTGCATCCTCTACATGATCTCCATT
 GTAGGTAACCTCAGCATTCTCACTCTGGTGTTTTGGGAGCCTGCTCTGCATCAGCCCATGT
 ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCACT
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT
 GTTCTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC
 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG
 55 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCACTCTCTTCCCTTTCCCTTTTGTGGT
 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA

TTTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC
 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA
 TCTGTGCAGTGCTGGCCTTTTATGTGCCATAATTGCTGTCTCCATGATTCACCGCTTCTGG
 AAAAGTGCTCCACCTGTTGTTTCATGTGTCATGTCCAATGTCTACCTGTTTGTACCACCCAT
 5 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

AOLFR144 sequences:

MGLFNVTHPAFFLLTGIPGLESSHWSLGPLCVMYAVALGGNTVILQAVRVEPSLHEPMYYFL
 10 SMLSFSDDVAISMATLPTVLRTECLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD
 PLRYATVLTTEVIAAMGLGAAARSFITLFLPLFLIKRPLICRSNVLSHSYCLHPDMMRLACADISI
 NSIYGLFVLVSTFGMDLFFIFLSYVLILRSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS
 TVHRFGKHVPCYIHVLMNSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

15 ATGGGGTTGTTCAATGTCACTCACCCTGCATTCTTCTCCTGACTGGTATCCCTGGTCTGGA
 GAGCTCTCACTCCTGGCTGTCAGGGCCCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA
 AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCCAGCCTCCATGAGCCCCATGTACTACT
 TCCTGTCCATGTTGTCTTTCAGTGATGTGGCCATATCCATGGCCACACTGCCACTGTACTC
 CGAACCTTCTGCCTCAATGCCCGCAACATCACTTTTGATGCCTGTCTAATTCAGATGTTTCT
 20 TATTCACCTTCTTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG
 TGGCCATTTGTGACCCCTTGCCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT
 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCCTTTTCCCTCTTCCCTTTCTTATTAAGA
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG
 AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTCTTGTATCCAC
 25 CTTTGGCATGGACCTGTTTTTATCTTCTCCTCTCCTATGTGCTCATTCTGCGTTCTGTCATGG
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTCACATATCCTGGC
 TGTACTTGCAATTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT
 GTCCCATGCTACATACATGTCCTCATGTCAAATGTGTACCTATTTGTGCCTCCTGTGCTCAA
 30 CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTCCGCATGTTTCAC
 CACATCAAAATATGA (SEQ ID NO: 266)

AOLFR145 sequences:

MSVQYSLSPQFMLLSNITQFSPIFYLTSPFGLGKHWIFIPFFFMVMVAISGNCFILIIKTNPRLH
 35 TPMYYLLSLLALTDLGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESSVLLMMSFD
 RFVAICHPLRYSVIITGQQVVVRAGLIVIFRGPVATIPVLLLKAFPYCGSVVLSSHFLHQVEVIQLA
 CTDTTFNLYGLMVVVFVMDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVLVF
 FVPMMLSLVHRFGKHAPPAIHLLMANVYLFVPPMLNPIIYSIKTKEIHRAIILKLLGLKKASK
 (SEQ ID NO: 267)

40 ATGTCAGTCCAATATTCGCTCAGTCCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG
 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG
 ACCAACCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT
 GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT
 45 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCCCTTCATGGAGTC
 CTCAGTGCTCCTCATGATGTCCTTTGACCGCTTTGTGGCCATCTGCCACCCCTCTGAGGTATT
 CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC
 TGTGGCCACTATCCCTATTGTCCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC
 TCTCCCACTCATTTTGCCTGCACCAAGGAGTACAGCTGGCCTGCACAGATACCACCTT
 50 CAATAATCTGTATGGACTGATGGTGGTAGTTTCACTGTGATGCTGGACCTGGTGTCTCATC
 GCACTGTCCTATGGACTCATCCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC
 GCCGTGCCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATTCTTTGTGCCCATG
 ATGGGGCTGTCCCTGGTGCACCGTTTTTGGGAAGCATGCCCCACCTGCTATTATCTTCTTAT
 GGCCAATGTCTACCTTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAGACC
 55 AAGGAGATCCACCGTGCCATTATCAAACCTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ
 ID NO: 268)

AOLFR146 sequences:

MSQVTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMFLSM
LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDCYVAICCP
5 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVCADIRLN
SWYGFALALLIIVDPLLIVISYTLILKNILGTATWAERLRALNNCLSHILAVLVLYIPMVGVSM
HRAKHASPLVHVIMANIYLLAPPVMNPPIYSVKNKQIQWGMLNFLSLKNMHSR (SEQ ID NO:
269)

10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG
GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGTCTGCTGTCTCTACACCATCTCCATC
ATGGGCAATACCACCATCTCACTGTCATTCGCACAGAGCCATCTGTCCACCAGCGCATGT
ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCTCACCACTACCCACA
GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAAGTACAGCTCTGAGGCCTGTTTGTCTCAGTT
15 TTTCTTCCTTCATGGATTCTCCTTTATGGAGTCTTCTGCTCCTGGCTATGTCCGTTGACT
GCTATGTGGCCATCTGCTGTCCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT
AGAACTGGGTTAGCCATCATTGTCTGCTGTGTTCTGGCGGTTCTTCCCTCCCTTTTCTTACT
CAAGCGACTGCCTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA
TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCTT
20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTTATTCTGAAAAATA
TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT
TCTAGCTGTCCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA
AGCATGCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCCGGT
GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTT
25 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

AOLFR147 sequences:

MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCIIYIVAVVGNICILLYLIVVEHSLHEPMF
FFLSMLAMTDLILSTAGVPKALSIFWLGAAREITFPGLTQMFFLHYNFVLDSAILMAMAFDHYV
30 AICSPLRYTTILTPKTIKSAMGISFRSFCILPDVLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI
NFWYGFCVPIMTVISDVILIAVSYAHILCAVFGLPSQDACQKALGTCGSHVCVILMFYTPAFFSI
LAHRFGHNVSRFTFHFIMFANLYIVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:
271)

35 ATGCCATCTGCCTCTGCCATGATCATTTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT
TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATTCCCTTCTGTATC
ATCTACATTGTAGCTGTTGTGGGAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA
GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC
ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTGGCTAGGGGCTCGCGAAATCACATTCC
40 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCTGCTGGATTACGCCATTCTG
ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATACCACCATCTT
GACTCCCAAGACCATCATCAAGAGTGCTATGGCATCTCCTTTTGAAGCTTCTGCATCATC
CTGCCAGATGTATTCTTGTGCTGACATGCCTTCTGCTGAGGACACGCATCATACCCACACA
CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG
45 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCTT
ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT
CGGCACTTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTCTCCA
TCCTCGCCCATCGCTTTGGACACAATGTCTCTCGACCTTCCACATCATGTTTGCCAATCTC
TACATTGTTATCCACCTGCACTCAACCCCATGGTTTACGGAGTGAAGACCAAGCAGATCA
50 GAGATAAGGTTATACTTTTGTCTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

AOLFR148 sequences:

MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYFLC
MLAGADIVLSTCTIPQALAIWFWRAGDISLDRCTQLFFIHSTFISEGILLVMAFDHYIAICYPLR
55 YTTILTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

FSILMSTVVLDDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCIILFYGSGIFTILTQRFGR
HIPPCIHIPLANVCILAPPMLNPIIYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

5 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTTCTTCAATTCCTATGTCAACGCCCTT
CTTGGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT
ACCTCTTCCTCTGCATGCTGGCTGGAGCAGACATTGTCTCTCCACGTGCACCATTCCTCAG
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT
CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC
10 ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCTTACAAATGCTCTGATCAA
GAAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT
TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCACACACCTTTTGTGAACACATTGG
CCTAGCCAAATATGCATGTAATGACATTGAATAAACATTTGGTATGGGTTTTCCATTCTA
ATGTGCGACGGTGGTCTTAGATGTTGTACTAATTTTTATTTCTATATGCTGATTCTCCATGC
15 TGTCTTCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTGGCTCCCATG
TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGA
CGCCACATTCCACCTTGTATCCACATCCCGTTGGCTAATGTCTGCATTCTGGCTCCACCTAT
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAATCCAGGAACAGGTGGTTCAGTTT
TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

20

AOLFR149 sequences:

MSNASLLTAFILMGLPHAPALDAPLFGVFLVYVLTVLGNLLILLVIRVDSHLHTTMYYFLTNL
SFIDMWFSVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSYP
LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLCDAPPILKLACADTS
25 AIETVIFVTVGIVASGCFVLIVLSYVSIVCSILRIRTSEGKHRAFQTCASHCIVVLCFFGPGLFIYLR
PGSRKAVDGVVAVFYTVLTPLLNPVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC
TGGACGCCCCCTCTTTGGAGTCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCCTCA
CCAACCTGTGCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC
TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTCT
TTCATTCTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGTCTGTGATCGCTACCT
35 GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG
GCCACGACACTGGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC
ATTTGCCCTACTGTGGACCCAACCTGGATCCAGCACTATTTGTGTGATGCACCGCCATCCT
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCT
40 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGAAAGC
TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCCCTTCTCAACCCTGTTGTGT
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC
ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

45

AOLFR150 sequences:

MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTTLLGNLLIMVTVTCESRLHTPMYFLLR
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLPLPFCGPNVLDTFYCDVPQVLKLTCTDTFA
50 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGRRKAISTCTSPHHCGDPAFCALHCLC
PALHCPPHRKGHLCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

55 ATGGAGTTGGGAAATGTCACCAGAGTAAAAGAATTTATATTTCTGGGACTTACTCAATCCC
AAGACCAGAGTTTGGTCTTGTCTTTCTTTTTTATGTCTTGTGTACATGACGACTCTGCTGGGA
AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCATGTACTTCCT
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACCTGCTCCTAAAGTCTTGC

TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT
 CTTCACCTCCTTGGTGGGGCAGACATTTTTTCTCTCTGTGATGGCGTTTGACTGCTACA
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT
 CATCTCTGCCTCTTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC
 5 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCCTC
 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTTCCAACAATGGCCTGGT
 CACTACCCTGTGGTTTATCTTCCTGCTTGTGTCCTACACAGTCATCCTAATGACGCTGAGGT
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGACCTCCCCACATCACTGTG
 10 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC
 AGAAAAGGCCATCTCTGTCACCTTCACTGTCTATCTCCCCTCTGCTGAACCCTTTGATCTACA
 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT
 CTGA (SEQ ID NO: 278)

AOLFR151 sequences:

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLRTNSHLQTPMYFFLGHLS
 FVDICYSSNVTPNMLHNFLEQKTISYAGCFTQCLLFIALVITEFYILASMLDRYVAICSPHY
 SRMSKNICVCLVTIPYMYGFLSGFSQSLLTFHLSFCGSLEINHFCADPPLIMLACSDTRVKKMA
 MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFSTCASHLTIVTLFYGTLCMYVRPSE
 KSVEESKITAVFYTLFSPMLNPLIYSLRNTDVLAMQMQMIRGKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCTTGCGATCTACCTAATCACACTGGCAGG
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCCACCTGCAAACACCCATGTATTTT
 25 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT
 GCACAATTTCTCTCAGAACAGAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT
 CTCTTCATCGCCCTGGTGATCACTGAGTTTTACATCCTTGCTTCAATGGCATTGGATCGCTA
 TGAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTTCTCTCAGTCACTGCTAACCTT
 30 TCACTTATCCTTCTGTGGCTCCCTTGAAATCAATCATTCTACTGCGCTGATCCTCCTCTTA
 TCATGCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT
 TAATCTCTCAAGCTCTCTCTTCATCATTCTTCTGCTCTATCTTTTCACTTTTGCAGCGACTT
 CAGGATCCGTTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCCACCTGACA
 ATAGTCACTTTGTTTTATGGAACCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAGT
 35 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTTGAGCCCAATGCTGAACCC
 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA
 AAATCCTTTCATAAAATGTCAGTTTAG (SEQ ID NO: 280)

AOLFR152 sequences:

40 MDQINHTNVKEFFLELTRSRELEFFLVVVFVAVYVATVLGNALIVVTITCESRLHTPMYFLLRN
 KSVLDIVFSSITVPKFLVDLLSDRKTISYNDMAQIFFHFAGGADIFFLSVMAYDRYLAIKPL
 HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT
 FALELFMISNGLVTLLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV
 YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSESARKWG (SEQ ID
 NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCTGGAACCTTACACGTTCCC
 GAGAGCTGGAGTTTTTCTTGTGTTGTGGTCTTCTTGCTGTGTATGTAGCAACAGTCCTGGG
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC
 50 TCCTGCGGAACAAATCAGTCCTGGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG
 GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT
 TCTTCCACTTTGCTGGTGGGGCAGATATTTTTTCTCTCTGTGATGGCCTATGACAGATAC
 CTTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC
 TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCAATCAATCATCCAGGTAATTCTGATGC
 55 TTCCATTTCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG
 GTAAACTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC
 TGGTGACCCTGCTCTGGTTCCTCCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG

AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCACATGCTG
GTGGTGACTCTTCACTTCGTGCCTTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCATGCTGAACCCCATCATC
TATTCCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG
5 CCTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

AOLFR153 sequences:

MSKTSLVTAFILTGPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL
10 RYTSMMMSGRCALLATSTWLSGLHSAVQILTFLHPYCGPNQIQHYLCDAPPILKLACADTSA
NEMVIFVDIGLVASGCFLILVLSYVSIVCSILRIHTSEGRHRAFQTCASHCIVVLCFFVXCVFIYLR
PGSRDVVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLKRDKVAHSQGE (SEQ ID NO:
283)

15 ATGTCCAAGACCAGCCTCGTGACAGCGTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCCACTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCATGTACTACTTCCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
20 TCCACTTCTGGGGAGCACCAGAGTGTTCCTCTACACAGTCATGTCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA
AACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT
25 GGCCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT
GGTCCTTTGCTTTTTTGTNNCCTGTGTTTTCATTTACCTGAGACCAGGCTCCAGGGACGTGC
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT
30 TCTCAGGGAGAATAA (SEQ ID NO: 284)

AOLFR156 sequences:

MCWAMPSPFTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFIYTFIIIDNLLIFSAVRL
DTHLGNPMYNFISIFSLEIWTATIPKMLSNLISEKKAISMTGCILQMYFFHSHLENSEGILLTT
35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGLILLPEIVMISTLPFCGPNQIQHIFCDLVP
VLSLACTDTSMILIEDVIHAVTHIITFLIALSYVRIVTVILRIPSSEGRQKAXSTCAGHLMVFLIFFG
SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPPIIYSLRNKDMNNAIKKLFCLQKVLNKPGG
(SEQ ID NO: 285)

40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA
ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT
CCTGTACTTCTTTCTTTACTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT
CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT
CCTTTCTGGAGATCTGGTACACCACAGCCACCATTCCCAAGATGCTCTCCAACCTCATCAG
45 TGAAGAAGAGGCCATCTCAATGACTGGCTGCATCTTGCAGATGTATTTCTTCCACTCACTT
GAAAACTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA
ACCCTCTTCGCTATCAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC
TGCCTCTTCGGTTTCTTATCCTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG
TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT
50 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTGATGCTGTGACCATCATCATTACCT
TCCTAATCATTGCCCTGTCCTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT
GAAGGGAGGCCAAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT
TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTTGGACAC
AGCCATTGCACTGATGTTTACTGTACTTGTCTCAATTTCAATCCCATCATTTATAGCCTGA
55 GAAACAAGGACATGAACAATGAATTAATAAACTGTTCTGTCTTCAAAAAGTGTGTAACA
AGCCTGGAGGTAA (SEQ ID NO: 286)

AOLFR157 sequences:

MAMDNVTAVFQFLIGISNYPQWRDFTFTLVLIYLSLTLGNGFMIFLIHFDPNLHTPIYFFLSNL
SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP
5 LRYSVVMNGPVCVCLVATSWGTSVLVTAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL
NEFMILITSIFTLLLPFGFVLLSYIRIAMAIIRISLQGRLEKAFSTTCGSHLTVVTIFYGSAISMYMKT
QSKSSPDQDKFISVFYGA LTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTAACTATCC
10 TCAATGGAGAGACACGTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG
AATGGATTTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT
CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG
TGCATTGTTTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTG
TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG
15 TTGCTATCAGCAATCCCCTGCGTTATTCACTGGTTATGAATGGCCCAGTGTGTCTGCTT
GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG
CTTCACCTTCTGTGGGGCTAATGTCATCAACCATTTTGCCTGTGAGATTCTCTCCCTCATTA
GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTCACCC
TGCTGCTACCATTTGGGTTTGTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG
20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCCTTTACCACATGTGGCTCTCACCTGACCGTGG
TGACAATCTTCTATGGGTCAGCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCCCTCCC
TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG
ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG
ACATGA (SEQ ID NO: 288)

25

AOLFR158 sequences:

MKAGNFSDTPEFFLLGLSGDPELQPILFMLFLSMYLATMLGNLLIILAVNSDSHLHTPMYFLLSI
LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP
LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFFCELAHILKLACSDVLIN
30 NILVYLVTSLGLGVPLSGIIFS YTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLSS
GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKMDMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTCAGGGGATC
CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCCCTGTCCATGTACCTGGCCACAATGCTGGG
35 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCACCTCCACACCCCATGTACTTCC
TCCTCTCTATCCTGTCCTTGGTCGACATCTGTTTACCTCCACCACGATGCCCAAGATGCTG
GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT
TTGTCCTGGTTTTTGTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT
TGTTGGCCATCTGTCAACCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG
40 CTGCTTCTGCTGTCCTTCATCGTTAGTGTCCTGGATGCTCTGCTGCACACGTTGATGGTGCT
ACAGCTGACCTTCTGCATAGACCTGGAAATTCCTCACTTTTCTGTGAACTAGCTCATATTC
TCAAGCTCGCCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTGTTGGTGACAGCCT
GTTAGGTGTTGTTCTCTCTCTGGGATCATATTTCTCTTACACACGAATTGTCTCCTCTGTCA
TGAAAATTCATCAGCTGGTGGAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT
45 CGTTGTTTCTTGTGTTTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT
CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC
ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAAACTAATATCTAG
GATACCATCTTCCATTGA (SEQ ID NO: 290)

AOLFR159 sequences:

MGPRNQTA VSEFLLMKVTEDELPKLPFSLFLSMYLVLTILGNLLILLAVISDSHLHTPMYFLLFN
LSFTDICLTTTTPKILVNIQAQNSITYTGCLTQICLVLFVAGLESCFLAVMAYDRYVAICHP
RYTVLMNVHFWGLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL
INNILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMPARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS
55 SAVAESSRITAVASVMYTVVPQMMNPFYISLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

ATGGGACCCAGAAACCAAACAGCTGTTTCAGAAATTTCTTCTCATGAAAGTGACAGAGGAC
 CCAGAACTGAAGTTAATCCCTTTACAGCCTGTTCTGTCCATGTACCTGGTCACCATCCTGG
 GGAACCTGCTCATTCTCCTGGCTGTCATCTCTGACTCCCACCTCCACACCCCATGTACTTC
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAACCACAACCACAGTCCCAAAGATCCT
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCCAGATCTGT
 CTTGTCTTGGTTTTTTGCTGGCTTGGAAGTTGCTTTCTTGACGTCATGGCCTACGACCGCTA
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT
 GCAGCTGTCCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTACAGGTC
 10 ATCAAGCTCGCCTGTTCTGACACCCTCATCAACAACATCCTCATATATTTTGCAAGTAGTGT
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTT
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC
 TGTTTTTTCCTTGTTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT
 CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC
 15 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATTGGTAG
 GCTGTTTCCTTTTAG (SEQ ID NO: 292)

AOLFR160 sequences:

MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLGLIEDPELPVLSFLSMYLVITLGNLLILL
 20 AVISDSHLHTPMYFFLSNLSFLDICLSTTTPKMLVNIQAQNRSITYSGCLTQICFVLFFAGLENC
 LLAAMAYDRYVAICHPLRYTVIMNPRLCGLLLLSLLTSVNVNALLLSLMVLRSLFCTDLEIPLFF
 CELAQVIQLTCSDTLINNILIYFAACIFGGVPLSGHLSYQITSCVLRMPASGKHKAVSTCGSHL
 SIVLLFYGAGLGVYISSVVDSPRKTAVASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

25 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAATTCCTTCTCCTGGGACTGATAGAGGAT
 CCGGAAGTGCAGCCCGTCTTTTACAGCCTGTTCTGTCCATGTACTTGGTCACCATCCTGGG
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCATGTACTTCT
 30 TCCTCTCCAATCTCTCCTTTTTGGACATTTGTTAAGCACAAACCAGTACCCAAAGATGCTG
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCCAGATCTGCT
 TTGTCTTGTTTTTTGCTGGCTTGGAATTTGTCTCCTTGACGAATGGCCTATGACCGCTAT
 GTGGCCATTTGTCACCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTGC
 TGATTCTTCTCTCTCTGTTGACTAGTGTTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTTG
 35 AGGCTGTCCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA
 TCCAAGTACCTGTTTCAGACACCCTCATCAATAACATCCTGATATATTTTGACGCTTGATA
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT
 GAGAATGCCATCAGCAAGTGGAAGCACAAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGTGTACATTAGTTCTGTGGTTACTGACTC
 40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCCC
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTCATAGGGAGG
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTACAGGTTTCTAGAGTAA (SEQ ID
 NO: 294)

AOLFR161 sequences:

45 MEPRNQTSASQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLIILAISIDSHLHTPMYFFLANL
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCCLIQMYFFHFFGIVDSVIIAMMA YDRFVAICHPLH
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR
 50 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKKAFTSCSSHL SVVALFYGTTIGVYLCF
 SSVLTTVKEKASAVMYTAVTPMLNPFYSLRNRLKGALRKL VNRKITSSS (SEQ ID NO: 295)

55 ATGGAACCAAGAAACCAAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCCACCTCCACACCCCATGTACTTCT
 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTCGCCTG
 CTGGTCGGCGCCCTCTGGGCGTTTTCTTGCTTCTCATCTCACTCACTCACATCCTCCTGATGGC
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC
 5 TCCGACTTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA
 TGAAGGTCCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCCACCTGTC
 TGTGGTTGCTCTCTTCTATGGGACCACCATTGGCGTCTATCTGTGTCCCTCCTCGGTCCTCA
 CCCTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCCATGCTGAATCC
 10 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG
 AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

AOLFR162 sequences:

MMRLMKEVRGRNQTEVTEFLLLGLSDNPDQLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH
 15 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA
 YDRYAAIWNPLLYPVLVSGRICFLLIATSFLAGCGNAAIHTGMTFRLSFCGSNRINHFYCDTPPL
 LKLSGSDTHFNGIVIMAFSSFIVISCMIVLISYLCIFIAVLKMPSSLEGRHKAFSTCASYLMAVTIF
 FGTLFMYLRPTSSYSMEQDKVVSFYTIVIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID
 NO: 297)

20 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT
 CTATATGGCAAACATGGTGGGCAATTGGGGATGATTGTATTGATTAAGATTGATCTCTGT
 CTCCACACCCCCATGTATTTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT
 25 TCCGTCCTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG
 GATGTGCTGCCAGTTCTACTTCTTTGGCTCCTTCCTGGGGACTGAGTGCTTCCTGTTGGCC
 ATGATGGCATATGACCGCTATGCAGCCATTTGGAACCCCTGCTCTACCCAGTTCTCGTGT
 CTGGGAGAATTTGCTTTTGTCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC
 CATAACATACAGGGATGACTTTTAGGTTGTCCTTTTGTGGTTCTAATAGGATCAACCAATTTCT
 30 ACTGTGACACCCCGCCACTGCTCAAACCTCTCTGCTCTGATACCCACTTCAATGGCATTGTG
 ATCATGGCATTCTCAAGTTTATTGTATCATCAGCTGTGTTATGATTGTCCTCATTTCCTACCT
 GTGTATCTTCTATTGCCGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC
 ACCTGTGCCTCTTACCTCATGGCTGTCAACATATTCTTTGGAACAATCCTCTTCATGTACTT
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA
 35 ATAATCCCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC
 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

AOLFR163 sequences:

40 MQRSNHTVTEFILLGFTTDPGMQLGLFVVLGVYSLTVVGNSTLIVLICNDSCLHTPMYFFTGN
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL
 LYAQAMSIKLCALLVAVSYCGGFINSSIITKKTFSNFCRENIIDDFCDLLPLVELACGEKGGYK
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFTSCSSHLTSVTLYYGSILYIYALPRS
 SYSFDMKIVSTFYTVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

45 ATGCAGAGGAGCAATCATACAGTGAAGTGTGTTTATACTGCTGGGCTTCACCACAGACCCA
 GGAATGCAGCTGGGCCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA
 ATAGCACCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC
 ACTGGAAATCTGTCGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGAGTCTTCTTCT
 50 CTGCAGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT
 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGATTGCTG
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTCTCAATCATACCAAGAAAACGTTTTTC
 CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTTGCTTCCCTTGGTGG
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA
 55 TGTCATCTGCCCCGAGTGCTCATCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA
 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT

GTCAC TTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG
ATCTACAGCCTAAGGAATAAGGATGTGAAAGAGGCTCTGAAAAAACTTCTCCATAA (SEQ
ID NO: 300)

5

AOLFR164 sequences:

MFLTERNTTSEATFTLLGFSDYLELQIPLFFVFLAVYGFSVVGNLGMIVIINKINPKLHTPMYFFLN
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTTELILFAVMAYDHFVAICNP
LLYTVAISQKLCAMLVVVLYAWGVACSLTLACSAKLKLSFHGFNTINHHFCELLSISLSPDSYL
10 SLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPSASGHRKVFTSCASHLTAITIFHGTLFLYCVF
NSKNSRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ
(SEQ ID NO: 301)

15 ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG
ATTACCTGGAAGTCAAATTCCCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG
GTAGGGAATCTTGGGATGATAGTGATCATCAAATAACCCAAAAATTGCATACCCCATGT
ATTTTTCTCTCAACCACTCTCCTTTGTGGATTCTGCTATTCTCCATCATTTGCTCCCATGA
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCAATTCATTCTCAGGATGTTTGGTGCAATT
CTTTTTCTTTTGCACCTTTGTAGTGACTGAATTAATTCTATTTGCGGTGATGGCCTATGACC
20 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCCAGAACTCTGTGCC
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG
CTTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTTCTTCTGTGAGTTATCCTCC
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC
TTTTAATGAGATAAGCACACTACTCATCTTCTGACATCTTATGCATTTCATCATTTGTCACCA
25 CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCACCT
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTACACCGTGGTGATCCCCTTGTGAA
TCCCCTGATCTACAGTCTGAGAAATAAAGATGTTAAGGATGCAATCCGAAAAATAATCAAT
ACAAAATATTTTCATATTAAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA
30 A (SEQ ID NO: 302)

AOLFR165 sequences:

MAVGRNNTIVTKFILLGLSDHPQMKIFLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL
SNLSFLDICYVSSSTAPKMLSDIITEQKTSIFVGCATQYFVFCGMGLTECFLLAAMAYDRYAAICN
35 PLYTVLISHTLCLKMVVGAYVGGFLLSFIETYSVYQHDFCGPYMINHHFFCDLPPVLALSCSDF
TSEVVTFIVSVVGVISVLVVLISYGYIVAAVVKISSATGRTKAFSTCASHLTAVTLFYGSGFFM
YMRPSSSYSLNRDKVVSIFYALVIPVNPPIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG
(SEQ ID NO: 303)

40 ATGGCTGTAGGAAGGAACAACAATTGTGACAAAATTCATTCTCCTGGGACTTTTCAGACC
ATCCTCAAATGAAGATTTTCCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC
TGGAAGTAAAGCCTCATTGCCCTCATTAAGATGGACTCTCACCTGCACATGCCCATGTACT
TCTTCCTCAGTAACCTGTCCTTCTGGACATCTGCTATGTGTCTCCACCGCCCTAAGATG
CTGTCTGACATCATCACAGAGCAGAAAACCAATTCCTTTGTTGGCTGTGCCACTCAGTACT
45 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCCCTCATATCCCATACTTTGTTTAA
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTCTTTCATTGAAACATACTCTGT
CTATCAGCATGATTTCTGTGGGCCCTATATGATCAACCACTTTTCTGTGACCTCCCTCCAG
TCCTGGCTCTGTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGTT
50 GTCGTTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT
TGTGAAGATCAGCTCAGCTACAGGTAGGACAAAGGCCTTCAGCACTTGTGCCTCTCACCTG
ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCCAGCTA
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCGTGGTGAAT
CCCATCATCTACAGTTTTAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA
55 AGGGACCCCGGGATTCTCACGGTGGACCATTCAATTTTATGACCTTGGGCTAA (SEQ ID
NO: 304)

AOLFR166 sequences:

MEMENCTRVKEFIFLGLTQNREVSLVFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH
NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL
5 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLLPLFCGPNVLDTFYCDVHRVLKLAHTDIFIL
ELLMISNNGLLTTLWFFLLLVSIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP
FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

10 ATGGAGATGGAAAACCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC
GGGAAGTGAGCTTAGTCTTATTTCTTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA
AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTTT
GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTCCATCACAGTGCCCAAGGTTCTGG
TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA
15 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG
TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATGCAATTGGGCT
CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTTGCTC
CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCTC
CAAACCTGGCCCATACAGACATTTTCTACTTGAACCTACTAATGATTTCCAACAATGGACTG
20 CTCACCACACTGTGGTTTTTCTGCTCCTGGTGTCTACATAGTCATATTATCATTACCCAA
GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCCACATCACTGT
GGTGACCCTGCATTTCTGTCCTGCATCTATGTCTATGCCCAGGCCCTTCACTGCCCTCCCA
TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC
ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCCT
TCTGATAGAAAATAG *SEQ ID NO: 306)

25

AOLFR167 sequences:

MSITKAWNSSSVTMFILLGFTDHPQLALLFVTFGLGIYLTTLAWNLAFLIRGDTHLHTPMYFF
LSNLSFIDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLLTAMAYDRYAAI
SSPLLYPTIMTQGLCTRMVVGAYVGGFLSLIQAASSIFRLHFCGPNIIINHFFCDLPPVLALSCSDT
30 FLSQVVNFLVVVTVGGTSFLQLLISYGYIVSAVLKIPSAEGRWKACNTCASHLMVVTLFGTAL
FVYLRPSSSYLLGRDKVVSFVSLVIPMLNPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID
NO: 307)

35 ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA
CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCTGGGCATCTATCTTACCACC
CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA
TGTACTTCTTCTAAGCAACTTATCTTTCATTGACATCTGCTACTCTTCTGCTGTGGCTCCC
AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC
40 AGTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCTCCTGACTGCTATGGCATA
GACCGATATGCAGCCATCTCCAGCCCCCTTCTCTACCCCACTATCATGACCCAGGGCCTCT
GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG
CTCCATATTTAGGCTTCACTTTTGGCGGACCCAACATCATCAACCACTTCTTCTGCGACCTCC
CACCAGTCTGGCTCTGTCTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCCTGCTG
GTGGTCACTGTGCGAGGAACATCGTTCTCCTCAACTCCTTATCTCCTATGGTTACATAGTGT
45 CTGCGGTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCCT
CGCATCTGATGGTGGTGACTCTGCTGTTTGGGACAGCCCTTTCTGCTGACTTGGCAGCCAG
CTCCAGCTACTTGCTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTGATTGGTGATCCCC
ATGCTGAACCCTCTCATTTACAGTTTGAAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG
GTGTTGGAAGGAAGAAAGTGTTCCTTAG (SEQ ID NO: 308)

50

AOLFR168 sequences:

MEKINNVTETIFWGLSQSPEIEKVCVVFVSFFYIIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV
DICYSSVTAPKMIVDLLAKDKTISYVGCMLQLLGVFHFGCTEIFILTVMAYDRYVAICKPLHYM
TIMNRETCNKMLLGTWVGGLHSHIIQVALVVQLPFCGPNEIDHYFCDVHPVLKLACTETIYIG
55 VVVTANSGTIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVIFFGPCTFMYMRPD

TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAAAAATAAACAAACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA
TTGAGAAAGTTTGTGTTTGTGGTGTGTTTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTTCTTTCTCAG
CTTCTGTCTTTTGTGGACATTTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC
TGTTAGCAAAGGACAAAACCATCTCCT1ATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC
ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT
10 ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGGAGACATGCAATAAAATGTTAT
TAGGGACGTGGGTAGGTGGGTTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACCT
ACCCCTTTTGTGGACCAATGAGATAGATCACTACTTTTGTGATGTTTACCCTGTGTTGAAA
CTTGCCTGCACAGAAACATACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG
CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAG
15 CAGTCAGCAGAAGGCAGGCGCAAAGCCCTCTCCACCTGTGGCTCCCACATTGCCATGGTGC
TTATCTTTTTTCGGCCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT
AAGATGGTGGCTGTATTTTACACCATTATCACTCCCATGTTAAATCCTCTGATTTATACACT
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA
GGCTAAAGGGAAATAG (SEQ ID NO: 310)

20

AOLFR169 sequences:

MMDNHSSATEFHLLGFPGSQGLHHILFAIFFFFYLVTLMGNTVIIIVIVCVDKRLQSPMYFFLSHL
STLEILVTTHVPMMLWGLLFLGCRQYLSLHVSINFSCGTMEFALLGVMAVDRYVAVCNPLRY
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI
25 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

ATGATGGACAACCACTCTAGTGCCACTGAATTCCACCTTCTAGGCTTCCCTGGGTCCCAAG
GACTACACCACATTCTTTTTGCTATATTCTTTTTCTTCTATTTAGTGACATTAATGGGAAAC
30 ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTCCT
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG
GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCTG
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT
35 CATGGGTGTTTGGATTTCTTTCTGAAATCTGGCCCATCTATGCCACATTTAGTTTACCTTC
CGCAAATCAAATTCATTAGACCATTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCCT
GCGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAATGGCTGTTTTTATTCTCATTGGT
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTACCTGTGTTGTGATTG
40 GCTATGGCAGCTGCTTGTGTTCTCTACGTGAAACCCAAAGCAAACACAGGGAGTTGAGTACAA
TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTCATCTTTACTCT
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT
GAAAGATTAG (SEQ ID NO: 312)

45 **AOLFR170 sequences:**

MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCLYLSVS
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTTHIVMVI
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDDLVPKVVITFTGCMVQFYFHFSLGSTSFLIL
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH
50 FFCDFNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG
SHLTLVFIGYSSTIFLYVRPGKAHSVQVRKVVALVTSVLTPFLNPFILFCNQTVKTVLQGMQ
RLKGLCKAQ (SEQ ID NO: 313)

ATGTCTTTCACTTCTCTCATACCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT
55 TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTTGCCTTT
CTCTCTCTATTCTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTC

TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTCTTCTTGCATGCAGGGCCCCATACTG
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG
 TGAGCTGCAGGCCCTTCTGTATGGCCCTTCTCATGCTTTATCTTCTCGCCTTCATGGGAA
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC
 5 CTGGGCAATTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGGCCAGGATGCTCT
 CAGACCTGTTGGTCCCCCACAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC
 CACTTTTCCCTGGGGTCCACCTCCTTCTCATCCTGACAGACATGGCCCTTGATCGCTTTGT
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG
 GCTGGGGCTGCCTGGGCAGCTCCTTTCCTAGCCATGGTACCCACTGTCTCTCCCGAGCTC
 10 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAAATGAACCTCTCCTG
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTCTGGGACTTTCTGATGGCCTTGACCTT
 TGTCTCAGCTCCTTCTGGTGACCCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC
 GGATCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTCTCCACTTGCGGGTCTCACCTCACACT
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT
 15 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTCTCAATCCCT
 TTATCCTTACCTTCTGCAATCAGACAGTTAAACAGTGCTACAGGGGCAGATGCAGAGGCT
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

AOLFR171 sequences:

20 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAIYSTAMSPKLMIDLLCDKIAISLSACMGQLFI
 EHLLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVAMIGGFVHSHVQIVFLYSLP
 ICGPNVIDHSVCDMYPLLELLCLDITYFIGLTVVANGGIIICMVIFTLISCVILNFKTYSQEER
 HKALPTCISHIIVVALVFVPCIFMYVRPVSNFPFDKLMTVFYSHITLMLNPLIYSLRQSEMKNAM
 KNLWCEKLSIVRKRVSPTLNIFIPSSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA
 TGACTTCTTCTTGCCTACTTGTCACTTATGGATGCCATATATTCCACTGCCATGTCACCC
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCCCTGTGAGCTTGCATGGGTC
 AGCTCTTCATAGAACACTTACTTGGTGGTGACAGAGGTCTTCCCTTTGGTGGTGATGGCCTA
 30 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT
 TGCATCCTTCTGTTGGTGGTGGCCATGATTGGAGGTTTTGTGCACTCTGTGTTCAAATTGT
 CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT
 ACCCATTTGTTGGAAGTGTGTGCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA
 TGGTGGAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA
 35 ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA
 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTTATGTATGTTAGACCCGTTTCCA
 ACTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCACACTGAACATATTTATTCTAGTTCTA
 40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTLVFGPIYLLALLGNGALPAVVWIDSTLHQPM
 FLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR
 45 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIVVPFLLVAKFEHFQAKTIGHTYCAHMAV
 VELVVGNTQATNLYGLALSIAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSHICVIL
 AFYIPGLFSYLAHRFGHHTVPKPVHILLSNIYLLPPALNPLIYGARTKQIRDRLLETFTFRKSPL
 (SEQ ID NO: 317)

50 ATGGCAGAAACTCTACAACCTCAATTCCACCTTCTACACCCAAACTTCTTCATACTGACTG
 GCTTTCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTATCT
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGGTGTGGATAGACTCCACACTGCA
 CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT
 55 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC
 CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC

AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC
CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA
TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCACTTATA
TGGTCTGGCACTTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT
5 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG
GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCCTAC
CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT
CTACTTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC
AGAGACCGACTCCTGGAAACCTTCACATTAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

10

AOLFR173 sequences:

MSHTNVTIFHPAVFVLPVIPGLEAYHIWLSIPLCLIYITAVLGNLSILVIVMERNLHVPMYFFLS
MLAVMDILLSTTTPVKALAFWLQAHNIAFDACVTQGGFFVHMMFVGESAILLAMAFDRFVAIC
APLRYTTVLTWPVVGRIALAVITRSFCIIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV
15 NIWYGFSVPVIMVILDVILIAVSYSILRAVFRLPQDARHKALSTCGSHLCVILMFYVPSFFTL
THHFGRNIPQHVHILLANLYVAVPPMLNPIVYGVKTKQIREGVAHRFFDIKTWCCTSPLGS
(SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTGCGCATCCCTGG
20 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTGCCTCATTACATCACTGCAGTCC
TGGGAAACAGCATCCTGATAGTGGTTATTGTCATGGAACGTAACCTTCATGTGCCCATGTA
TTTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG
CCCTAGCCATCTTTGGCTTCAAGCACATAACATTGCTTTTGATGCCTGTGTACCCAAAGGC
TTCTTTGTCCATATGATGTTTGTGGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG
25 CTTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG
AGGATTGCTCTGGCCGTCATCACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT
GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCCCTCACTCCTACTGTGAGCATATTGGA
GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTGGGTATGGCTTCTCAGTGCCCAT
TGTCATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG
30 TGTTCGTTTGGCCTCCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCACCT
CTGTGTCATCCTTATGTTTATGTTTCCATCTTCTTACCTTATTGACCCATCATTTTGGGCG
TAATATTCTCAACATGTCCATATCTTGCTGGCCAATCTTATGTGGCAGTGCCACCAATGC
TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCACCGGTT
CTTTGACATCAAGACTTGGTGCTGTACCTCCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35

AOLFR175 sequences:

MHFLSQNDLNINLPHLCLHRHSVIAGAFTIHRHMKIFNSPSNSSTFTGFILLGFPCPREGQILLFV
LFTVVYLLTLMGNNGSIICAVHWDQRLHAPMYILLANFSFLEICYVTSTVPSMLANFLSDTKIISF
SGCFLOFYFFFSLGSTECFFLAVMAFDRLAICRPLRYPTIMTRRLCTNLVVNCWVLGFIWFLIPI
40 VNISQMSFCGRSRIIDHFLCDPAPLLTLCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVRAVL
RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLNPIV
YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG
45 TCATTCAGTAATTGCTGGTGCTTTTACAATTACAGGCACATGAAAATCTTCAACAGCCCC
AGCAACTCCAGCACCTTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC
AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCTCATGGGCAATGGTTCC
ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA
ACTTCTCCTTCTTGGAGATATGTTATGTACCTCCACAGTCCCCAGCATGCTGGCCAACTTC
50 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCCTCCAGTTCTACTTTTTCTTCTCC
TTGGGCTCTACAGAATGCTTTTCTGCGCAGTTATGGCATTGATCGATACCTTGCCATCTG
TCGGCCTCTACGCTATCCAACCATATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT
GCTGGGTACTTGGTTTCATCTGGTCTTGAATCCTATCGTCAACATCTCCCAAATGTCCTTC
TGTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG
55 CAAAAAAGGCCCTGTGATAGAGCTTGCTTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC
TCTTCTCTTCATTGTGGGGTCCTATGCTCTGGTCGTGAGAGCTGTGTTGAGGGTCCCTTCA

5 CGAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCACCACCTAAGAATGAAGCTGGAAAGC
AGAAGACTGTGACTCTGTTTTATTCTGTTGTTACCCCACTGCTTAACCCGTGTGATATATAGT
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTGGGGAACATAA (SEQ ID NO:
322)

AOLFR176 sequences:

10 MFFIIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGGQREMQSCFFSFILVLYLLTLLNGAIVC
AVKLDRLHTPMYILLGNFAFLEIWIYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTTTECF
LSVMAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGFLCYPVPIVLISQLPFCGPNIIDHLVCD
PGPLFALACISAPSTELICYTFNSMIIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV
VSLFYGTLMVMYVSPTSNGNPAGMQKIITLVYTAMTPFLNPLIYSLRNKDMKDALKRVLGLTVS
QN (SEQ ID NO: 323)

15 ATGTTCTTTATTATTTCATTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG
CAGAGCTGCTTCTTCTCATTTCATCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC
TATTGTCTGTGCAGTGAAATTGGACAGCGCGCTCCACACACCCATGTACATCTTCTGGGA
AACCTTGCTTTCTAGAGATCTGGTACATTTCTCCACTGTCCCAACATGCTAGTCAATAT
20 CCTCTCTGAGATTAAAACCATCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTTC
ACTGGGTACAACAGAGTGTTTCTTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTCCCT
25 TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCATTGTTTGCAGTGGC
CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC
TCTGGTGCTGGTCTGAACTAAAGCTTTCTCCACATGTGGGTCCCACTAATGGTGGTGTCTC
TATTCTATGGAACCCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCTTATCTAT
30 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCCTGGGGTTAACAGTTAGC
CAAACTGA (SEQ ID NO: 324)

AOLFR177 sequences:

35 MSFFFVDLRPMNRSATHIVTEFILLGFGPCWKIQIFLSLFLVIYVLTLLNGAIIYAVRCNPLLH
TPMYFLLGNFAFLEIWIYVSSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTTECLFLAVMAYD
RYLAICHPLQYPAIMTVRFGKLVSFCLWIGFLGYPIPIFYISQLPFCGPNIIDHFLCDMDPLMAL
SCAPAPITECIFYTQSSLVLFFTSMYILRSYILLTAVFQVPSAAGRRAKAFSTCGSHLVVVSIFYG
TVMVMYVSPTYGIPTLLQKILTLVYSVTTPLFNPLIYTLRNKDMKLALRNVLFGMRIRQNS
(SEQ ID NO: 325)

40 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG
AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTGAGATTTTCTCTTCTCATTGTTT
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAGTGAGATGCA
45 ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTTGCCTTCTTGAGATCTGG
TATGTGTCTCCTCACTATTCTAACATGCTAGTCAACATTCTCTCCAAGACCAAGGCCATCTC
ATTTTCTGGGTGCTTCTCCTCCAGTTCTATTCTTCTTTTCACTGGGAACAACCTGAATGTCTCT
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCTGC
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTGG
GATACCAATTCCCATTTTCTACATCTCCCACTCCCTTCTGTGGTCTTAATATCATTGAT
50 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCACTAAGT
AATGTATTTTCTATACTCAGAGCTCCCTTGTCTCTTTTCACTAGTATGTACATTCTTCGA
TCCTATATCCTGTTACTAACAGCTGTTTTTCAGGTCCCTTCTGCAGCTGGTCGGAGAAAAG
CCTTCTCTACCTGTGGTTCTCATTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA
ATGTATGTAAGTCCTACATATGGGATCCCACTTTATTGCAGAAGATCCTCACACTGGTAT
55 ATTCAGTAACGACTCCTCTTTTAACTCTGATCTATACTCTTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCTGTTTGAATGAGAATTCGTCAAATTCGTGA (SEQ ID NO: 326)

AOLFR178 sequences:

5 MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP
LQYLTIMSPRMCMFFLVAAWVTGLIHSVVQLVFVNLPCGPNVSDSFYCDLPRFIKLACTDSY
RLEFMVTANS GFISLGSFFILIISYVVILTVLKHSSAGLSKALSTLSAHVSVVVLF FGPLIFVYTW
PSPSTHLDKFLAIFDAVLTPVLNPIIYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTGTCAGAGTTTGTGTTCTCTGGGACTCACCAATTCCT
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTTACATGGCCAGTATGATGGGA
AACTCTCTCATTTTGTCTCACTGTGACTTCTGACCCTCACTTGCACTCCCCCATGTATTTTCT
GTTAGCCAACTCTCCTTCACTGACCTGGGTGTTTCTCTGTCACTTCTCCAAAATGATTT
15 ATGACCTGTTCAGAAAGCACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT
CATCCACGTCATTGGCGGTGTGGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAT
GTGGCCATATGTAAGCCCCCTCCAGTACCTGACCATTATGAGCCCAAGAATGTGCATGTTCT
TCTTAGTGGCTGCCTGGGTGACCGGCTTATCCACTCTGTAGTTCAATTGGTTTTGTAGTA
AACTTGCCCTTCTGTGGTCCTAATGTATCGGACAGCTTTTACTGTGACCTTCCTCGGTTTCAT
20 CAAACTTGCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTC
ATCTCTCTGGGCTCCTTCTTCACTGATCATTTCCTATGTGGTCATCATTCTCACTGTTCT
GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCCTTTCAGCTCACGTCAGTGTG
GTAGTTTTGTCTTTGGTCCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCCTCACTCCTGTTTTAAATCCTATCATCTACA
25 CATTAGGAATTGA (SEQ ID NO: 328)

AOLFR179 sequences:

MNGMNHSSVSEFVFMGLTNSREIQLLLFVFSLLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP
30 LHYLTIMSPRMCLYFLATSSIIGLIHSVLVQLVFVVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL
EFMVTVNSGLISVGSFVLLVISYIFILFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW
PSPTSHLDKYLAIFDAFITPFLNPVIYTFRNKDMKVMRRLCSRLAHFTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC
GGGAGATTCAGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA
AACCTTGTCAATTGTATTCACTGTAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCTT
CCTGGCTAACCTCTCAATCATTGATATGGCATTTTGCTCAATTACAGCCCCTAAGATGATTT
GTGATATTTTCAAGAAGCACAAAGGCCATCTCCTTTGCGGGATGTATTACTCAGATCTTCTT
TAGCCATGCTCTTGGGGGCACTGAGATGGTGCTGCTCATAGCCATGGCCTTTGACAGATAC
40 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT
TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA
GATTTACCTTTTTGTGGTCCTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT
CAGACTTGCTGTACCAACACCCAAGAACTGGAGTTCATGGTCACTGTCAATAGTGGACTC
ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCTACATCTTCATTCTGTTCACTGTTTG
45 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTCAGCTCATGTCAGTGTG
GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT
GGATAAATATCTTGCTATTTTTGATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA
CATTAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT
TTACAAAGATTTTGTA (SEQ ID NO: 330)

50

AOLFR180 sequences:

MTNKMAYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSSNFLLTAFPGLECAHVWISIPVCCLYTI
ALLGNSMIFLVIITKRLHKKPMYYFLSMLAAVDLCLTITLPTVLGVLWFHAREISFKACFIQMF
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF
55 HGGHELHSPFCYHPEVIKYTYSKPWISSFWGLFLQLYLNGLDVLFILFSYVLILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLLPPVLNPIIYSLKTKTIR
QAMFQLLQSKGSWGFNVRLGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCTCATAGT
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCTCAAACCTTCC
TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT
CTCTACACCATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTTCATCATTACTAAGCGGA
GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC
ATTACGACCCCTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCGGGAGATCAGCTTTAA
10 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCCCTCGGTGCTGG
TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC
ACAGACAGGATGGTCTGCTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC
TTCCCCTTCTTGAGCCATAAACACTGTGTCTTTTCATGGGGGTCACGAGCTTTCCCATCCA
TTTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT
15 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTTCTCCTAT
GTCCTGATCCTCCGTAAGTGTCTGGGCATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA
GCACTTGTGTCTGTACATCTGTGCAGTCACTATTTTCTATGTGCCACTGATCAGCCTCTCT
TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGTCTGTAGCACTTTGGCCAATATTTA
TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATCCGC
20 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTTCATGGGGTTTTAATGTGAGGGGTCTTA
GGGAAGATGGGATTGA (SEQ ID NO: 332)

AOLFR181 sequences:

25 MSVLNNSEVKLFLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMYYFLAML
AVSDMGLSLSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV
IYGFFIALCTMLDLALIVLSYVLILKILSIASLAERLKAALNTCVSHICAVLTFYVPIITLAAMHFF
AKHKSPLVILIADMFLVPLMNPIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCTTCTGATTGGGATCCCAGGACTGG
AACATGCCCACATTTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC
AACTGCACCATTCTCTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATTT
CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCTTACCATGTTGA
GGGTCTTCTTGTTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCTTC
35 ATTCATGGATTCACTGTGATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT
TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAAAT
GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTACCTTAAGGAG
ATTAATAATATTGTCAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA
AGCTGGCCTGCTCTGACAACAAGACCAATGTCTATGGCTTCTTCATTGCTCTCTGTACT
40 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCACATCTGTGCTGTG
CTCACCTTCTATGTGCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA
GCCCTCTTGTGTGATCCTTATTGCAGATATGTTCTTGTGTTGGTGGCGCCCTTATGAACCCC
ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT
45 GTATGTGGGAGATAA (SEQ ID NO: 334)

AOLFR182 sequences:

MTLGLSGNSSSSVSATFLLSGIPGLERMHIWISIPLCFMYLVSIPGNCTILFIKTERSLHEPMYLFL
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP
50 LHYVSILTNTVIGRIGLVSLGRSVALIFPLPFLMKRFPYCGSPVLSHSYCLHQEVMKLACADMK
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVYSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

55 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT
GTTTTCCATCCCGGGCAACTGCACAATTCTTTTTATCATTAACAGAGCGCTCACTTCAT

GAACCTATGTATCTCTTCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC
TCTCCCTACAGTCTGGGCATCTTTTGGGTTGGAGCACGAGAAATTAGCCATGATGCCTGC
TTTGCTCAGCTCTTTTTCATTCACTGCTTCTCCTCCTCGAGTCCTCTGTGCTACTGTCTATG
5 GCCTTTGACCGCTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC
AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTCGTAAGTGTAGCACTCATTTTTCCATTA
CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT
CCACCAAGAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT
GTTTGTTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA
10 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG
TGTTTTCCACATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC
ATCGCTTTGGAAGCAGGCACCCACCTGGTCCAGGTGGTTCATGGGTTTCATGTATCTTCT
CTTCTCCTCTGTGATGAATCCCATTTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA
GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGIPGTPDKNPWLAFLPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYYYFL
SILALTDVLSMSLTPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGLVSMADFDRFVAIRN
PLHYVSILTHDVIRKTGISVLTRAVCVFVPVFLIKCLPFCHSNVLSHSYCLHQNMMLACASTR
20 INSLYGLIVIFTLGLDVLLTLLSYVLTLLKTVLGIVSRGERLKTLLSTCLSHMSTVLLFYVPMGA
ASMIHRFWEHLSPVVHVMADIYLLLPVLPNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACCTGAATGCATCACAGGCCAACCCACCGTAACTTCATTCTGACAGGTATCCCAG
GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCTGGGATTCTCTACACACTCACACT
25 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCCACG
TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC
ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTGATGCATGCATCATGCAGAT
GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTTGAC
AGATTTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTCCG
30 AAAGACTGGAATATCTGTCCTCACCCGGGCAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT
ATAAAGTGCCTACCCTTCTGCCATTCCAATGTCTTGTCTCATTCACTGTCTTACACAAA
CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGT
ATCTTCACACTGGGGCTCGATGTTCTCCTCACTCTACTGTCTTATGTACTCACCTGAAGAC
TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCTCAGCACATGCCTCTCTCAC
35 ATGTCTACCGTGCTCCTCTTCTATGTTCTTTTATGGGTGCTGCCTCCATGATCCACAGATT
TTGGGAGCATTATACACAGTAGTGCACATGGTCATGGCTGATATATACCTACTGCTCCCG
CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

AOLFR184 sequences:

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIHALQPALHR
40 PMHFFLFLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVFVSMESSVLLAMSID
RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL
ACPEAWGAAYSLFVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHL SAVLLF
YIPMILLALINHPPELITQHTHTLLSYVHFLPLINPILYSVKMKEIRKRLNRLQPRKVGGAG
50 (SEQ ID NO: 339)

ATGTCAACATTACCAACTCAGATAGCCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT
TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC
TGTCTACCTTCTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC
50 GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTTGTCTAGTGTGTCTGATATTGGATTGGT
CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTGCTGGTGCTCACACTGTCCCTGCC
TCAGCCTGCCTTCTACAGATGGTTTTTATCCATGTCTTTTCTGTCTATGGAGTCCTCTGTCTT
GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC
CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC
55 ATCTGCCCCTGCCATTCTGCTGGCCTACATGCCCTACTGCCTCCCACAGGTCCCTAACCCAT
TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCCAGAAGCTTGGGGTGCAGCCT
ACAGCCTATTTGTGGTTCTTTTCAGCCATGGGTTTGGACCCCTGCTTATTTTCTTCTCCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT
CAAACCTGTGCTGCCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC
ATTTCTTCTTCCCTCCATTGATAAACCTATTCTCTATAGTGTCAAGATGAAGGAGATTAGA
5 AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:
340)

AOLFR185 sequences:

MFYPILNDISTKNNNSNIMSCCNILFIKTVEIILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR
10 VDCVPSRDHINQSMVLASGNSSSHPVSFILLGIPGLESFQLWIAFPFCATYAVAVVGNITLLHVIR
IDHTLHEPMYFLAMLAITDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHAFSSVESGVL
MAMALDCYVATCFPLRHSSILTPSVVIKLGATIVMLRGLLWVSPFCFMVSRMPFCQHQAIPQSYC
EHMAVLKLVCADTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA
SHICVILALYIPALFSFLTYRFGHDVPRVVHILFANLYLLIPPMLNPIYGVRTKQIGDRVIGCCG
15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTATGTT
GTAACATATTATTTATTAACAGTTGAAATTATTCTAGTTTATAATCAAACCCAATCACC
CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAATAACACTTGTTTTGATTGTT
20 ATCATCTGCAGAGAGTAGATTGCGTTCCCAGCAGAGACCATATTAACCAGTCCATGGTGCT
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCTTCTCATCCTGCTTGGAATCCCAGGCCTG
GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCCACTCAACCTAAGATGTT
25 GGCCATATTCTGGTTTCATGCTCATGAGATTCACTACCATGCCTGCCTCATCCAGGTGTTCT
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC
GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTCGTGATCAAAC
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCCTTCTGCTTCATGGTGTC
TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG
30 CTGAAGTTGGTGTGTGCTGATACAAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT
CTGTGGCTGGCTTTGATGATTGTGCTATTGCTATGTCATACGTGATGATTTTGAGAGCTGT
GCTTCAGTTGCCCTCAGGTGAAGCCCCCTCAAAGCTTTTAGCACACGTGCCTCCCATATC
TGTGTCTATCTGGCTCTTTATATCCCAGCCCTTTTTTCTTTCTCACCTACCGCTTTGGCCAT
GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT
35 CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

AOLFR186 sequences:

MSNASLVTAFILTGPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNLS
40 FIDMWFSTVTPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISSPL
RYTSMMSGSRCALLATGTWLSGSLHSAVQILTFLHPYCGPNQIQHYFCDAPPILKLACADTSA
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRRTSDGRRRAFQTCASHCIVVLCFFVPCVVIYLR
PGSMDAMDGVVAIFYTVLTPLLNPVYTLRNKEVKKAVLKLKRDKVAHPQRK (SEQ ID NO:
343)

45 ATGTCCAACGCCAGCCTCGTGACAGCATTCATCCTCACAGGCCTTCCCCATGCCCCAGGGC
TGGACGCCCTCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCTCTCA
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAAATGCTGATGAC
50 CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT
TCCACTTCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG
CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTCCAT
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA
55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT
GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT
GGTCCTTTGCTTCTTTGTTCCCTGTGTTGTCATTTATCTGAGGCCAGGCTCCATGGATGCCA
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGTAC
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT
5 CCTCAGAGGAAATAA (SEQ ID NO: 344)

AOLFR187 sequences:

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGIPGLEQLHIWLSIPFCIMYIAALEGNGILI
CVILSQAILHEPMYIFLSMLASADVLLSTTTPKALANLWLGYSHSIFDGLTQKFFIHLFIHSA
10 VLLAMAFDRYVAICSPRYVTILTSKVIGKIVTATLSRSFIIMFPSIFLLEHLHYCQINIAHTFCEH
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV
ILLFYVPALFSVFAYRFGRSIPCYVHILLASLYVVIPPMNLNPVIYGVRTKPILEGAKQMFNSLAK
GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG
CTATGAACAACTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA
GCAACTACATATCTGGCTGTCCATCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC
AATGGCATCCTAATTTGTGTCATCCTCTCCAGGCAATCCTGCATGAGCCCATGTACATAT
TCTTATCTATGCTGGCCAGTGCTGATGTCTTGCTCTCTACCACCACCATGCCTAAGGCCCTG
20 GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTTGATGGCTGCCTCACTCAAAAAGTTCTT
CATTCACTTCCTCTTCATTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG
CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC
TGCACTATTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA
25 TCTGTCCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTTGGCAGCTGCTCTTCTCTCCA
CAGGCCTGGACATCATGCTTATTACTGTTTCCTACATCCACATCCTCCAAGCAGTCTTCCGC
CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTCAT
CCTACTCTTCTATGTCCCTGCCCTTTTTTCTGTCTTTGCCTACAGGTTTGGTGGGAGAAGCA
TCCCATGCTATGTCCATATTCTCCTGGCCAGCCTCTACGTTGTATTCTCCTATGCTCAAT
30 CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTTCA
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

AOLFR188 sequences:

MFPSLCPCVLLVQLPLMNENMQCFVFCSDSLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN
35 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCRRLRHLSPPTSEEHMKNKNNVTEFILL
GLTQNPGEQKVLVFTFLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNRRCVCL
MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTGLSMIANGGAIC
AVTFFITLLSYGVILHSLKTQSLEGKRKAFYTCASHVTVVILFFVPCIFLYARNSTFPIDKSMTV
40 VLTFITPMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCACTTATGAATGAGAACAT
GCAGTGTTTTGTTTTCTGTTCTTGATAGTTTGCTGAGAATGATGGTTTCCCGCTTCATCC
45 ATGTCCCATTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC
TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCTTTGTTTGTAGGC
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAAACATGTGACTG
AATTTATCCTCTTAGGGCTCACACAGAACCCTGAGGGGCAAAAGGTTTTATTTGTACATT
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATCATGGCC
50 AGCCAGTCCCTGGGTTCCCCCATGTACTTTTTTCTGGCTTCTTTATCATTCATAGATACCGT
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATT
CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTATTTGCTGGTGCTGAAGTCATT
CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA
TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT
55 TCACTCATTGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCAATTG
ACAACTTCTGTGTGATTGTATCCCTTATTGAACTTGCTTGCACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTTGTGCTGTACCTTCTTCACTATCCTGC
 TTTCTATGGGGTCAATACACTCTCTTAAGACTCAGAGTTTGAAGGGAAACGAAAAGC
 TTTCTACACCTGTGCATCCCACGTCACTGTGGTCATTTTATTCTTTGTCCCTGTATCTTCTT
 GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA
 5 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT
 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA
 (SEQ ID NO: 348)

AOLFR189 sequences:

10 MQQNSVPEFILLGLTQDPLRQKIVFVIFLYMGTVVGNMLIIVTIKSSRTLGSMPYFFLFYLSF
 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDRYVAICKPLRYP
 TIMSQVQCILIVLAWIGSLIHSTAQIILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL
 VNSGAICSSSFMIISIYIVILHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFIYTRPPTTFPMD
 KMAVAFYITIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA
 GGCAGAAAATAGTGTGTTGTAATCTTCTTAATTTTCTATATGGGAAGTGTGGTGGGGAATAT
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA
 TTTTATTGTCTCTTGCAGATTCTTGTCTTTCAACTTCCACAGCCCCTAGATTAATTGTGGA
 20 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTGCACATA
 CATTTATTGTGGCTGCATGGAGATCTTTGTCTCATTCTCATGGCTGTTGATCGCTATGTGGC
 CATCTGTAAGCCCTTGCCTTACCAACCATCATGAGCCAGCAGGTCTGCATCATCTGATT
 GTTCTTGCCTGGATAGGGTCTTTAATACTCTACAGCTCAGATTATCCTGGCCTTAAGATT
 GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTTGCAGCCCTTGTGAAAC
 25 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG
 CTCAAGTAGTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCATTCACTGAGAAACC
 ACAGTGCCAAAGGGGAAGAAAAAGGCTCTCTCCGCTTGCACGTCTCACATAATTGTAGTCAT
 CTTATTCTTTGGCCCATGTATATTCATATATACACGCCCCCGACCACTTTCCCCATGGACA
 AGATGGTGGCAGTATTTTATACTATTGGAACACCCCTTCTCAATCCACTCATCTACACATCT
 30 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

AOLFR190 sequences:

MQRSNHTVTEFILLGFTTDPGMQLGLFVVLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN
 LSFLDLWYSSVHTPKILVTCISEDKSISFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL
 35 YAQTMPRRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPVLKLACSVRESYQ
 AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPPSS
 YSLKRDKMVSTFYTMLFPMNLNPMIYSLRSKDKMDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGAAGTTCATCCTGCTGGGCTTACCACAGATCCAG
 40 GGATGCAACTGGGCTCTTTGTGGTGTTCTGGGTGTGACTGTCTGACTGTGGTAGGAAG
 TAGCACCTCATCGTGTGATCTGTAATGACTCCCGCTACACACACCCATGTATTTGTCA
 TTGGAATCTGTCAATTTCTGGATCTCTGGTATTCTTCTGTCCACACCCCAAAGATCCTAGTG
 ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCACTTCTCTCTGC
 CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC
 45 ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT
 ATATTCCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTCACATTG
 GATTTTGTGGTGACAATGTCAATTGATGACTTTTCTGTGATGTTCCACCCCTCGTGAAGCT
 GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCTTCTGGCCTCCAATGTC
 ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT
 50 CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA
 CCTTATACTATGGCTCCATTCTCTACAACACTACTCCCGGCCAAGTCCAGCTACTCCCTCAAG
 AGGGACAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCCATGTTGAATCCCATGATCTA
 CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA
 (SEQ ID NO: 352)

55

AOLFR191 sequences:

MTGGGNITEITYFILLGFSDFPRIIKVLFTIFLVIYITSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS
FIDVCYISSTVPKMLSNLLQEQQTITFVGCIHQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS
SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLILSCTDTFFVQV
5 MTAILTMFFGIASALVIMISYGYIGISIMKITSKGSFKAFNTCASHLTAVSLFYTSGIFVYLRSSS
GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT
TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC
10 TGGAACTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT
CTTCCCTCAGTAACCTGTCCTTCATAGATGCTGCTATATCAGCTCCACAGTCCCCAAGATGC
TCTCCAACCTCTTACAGGAACAGCAAACCTATCACTTTTGTGTTGTATTATTACAGTACTTT
ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT
ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTCAACCCACCTCTGTGTTTGG
15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATTGGTGCTTTTGT
TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAACTGT
TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTC
TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA
TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTC AACACCTGTGCTTCTCATCTAAC
20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT
CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC
TTGATTTACAGTTTGAGGAACAAAGAAATTAAAGATGCCTTAAAGAGGTTGCAAAAGAGA
AAGTGCTGCTGA (SEQ ID NO: 354)

AOLFR192 sequences:

MENNTEVTEFILVGLTDDPELQIPLFIVFLFIYLITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV
DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMAYDRY AALCKPLHY
TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCSRNVVEHFFCDAPLLTLSCSDNYISEM
VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPEGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS
30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA
CTGCAGATCCCCTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT
GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCTCA
35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG
GTTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATTCTTCTTCTTTG
TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC
ATTGTGTAAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC
ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATT CATACTGGGAACACTTTCAGGC
40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGACT
CTCTCATGTTTCAGACAACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG
ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG
ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG
TTTCCATCTTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG
45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG
TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA
AGGCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

AOLFR193 sequences:

MENKTEVTQFILLGLTNDSELQVPLFITFPFIYIITLVGNLGIIVLIFWDSCLHNP MYFFLSNLSLV
DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYIFVAFATVENYLLASMAYDRYAAVCKPLHY
TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLSFCKSNEVHHFFCDIPAVMVLSCSDRHISEL
VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIAVGIFYGTIIFMYLQSSSH
SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSAFKKVVEKAKLSVGWSV (SEQ ID NO:
55 357)

ATGGAATAAGACAGAAGTAACACAATTCATTCTTCTAGGACTAACCAATGACTCAGAA
 CTGCAGGTTCCCCTCTTTATAACGTTCCCCTTCATCTATATTATCACTCTGGTTGGAAACCT
 GGGAATTATTGTATTGATATTCTGGGATTCTGTCTCCACAATCCCATGTACTTTTTTCTCA
 5 GTAACCTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA
 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT
 AGCTTTTGGCACTGTGGAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA
 GTGTGCAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA
 TAGGCTCCTACCTCTGTGGTTTCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC
 10 TCTTTCTGTAAGTCCAATGAAGTCCATCACTTTTTCTGTGATATTCCAGCAGTCATGGTTCT
 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTCTTATTTATGTTGTGAGCTTCAATATCT
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCAATCCCATGCTGAACCCTCTGGTCTA
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

AOLFR194 sequences:

20 MERQNQSCVVEFILLGFSNYPELQGQLFVAFLVIYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL
 SVVDLSFSAVIMPEMLVVLSTEKTISFGGCFQMYFILLFGGAECFLLGAMAYDRFAAICHPL
 NYQMIMNKGVFMKLIIFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTFL
 FEIYAFTGTFLIILVPFLLILLSYIRVLFAILKMPSTTGRQKAFSTCAAHLTSVTLFYGTASMTYLQ
 PKSGYSPETKKVMSLSYSLLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO: 359)

25 ATGGAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC
 CTGAGCTCCAGGGGCAGCTCTTTGTGGCTTTCCTGGTTATTTATCTGGTGACCCTGATAGG
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT
 30 TTCTCCTGAACCTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT
 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT
 TTCATCCTTCTTTTGGTGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT
 TGCTGCAATTGGCCTCTCTCAACTACCAAATGATTATGAATAAAGGAGTTTTATGAAA
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT
 35 TAGAACTTGCATGTGCAGACACGTTTTTGTGAAATCTATGCATTCACAGGCACCTTTTTG
 ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTTCGAGTTCTGTTTGCATCCTG
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC
 ACCGGAACCAAGAAAGTGATGTCATTGTCTTACTCACTTCTGACACCACTGCTGAATCTG
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

AOLFR195 sequences:

45 MIVQLICTVCFLAVNTFHVRSFDLKAADDMEINQTLVSEFLLGLSGYPKIEIVYFALILVMY
 LVILIGNGVLIASIFDSHFHTPMYFFLGNLSFLDICYTSSSVSTLVSLISKRNISFSGCAVQMFF
 GFAMGSTECLLLGMMAFDRYVAICNPLRYPIILSKVAYVLMASVSWLSGGINSVQTLAMRL
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVLPLMVIFFSYMFIYTLQMNSATG
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEELQALDKLISLFYGVVTPMLNPILYSR
 NKDVKAADV KYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTCAAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC
 TTCTTTTGAATTCCTGAAAGCAGATGACATGGGTGAGATTAACCAGACACTTGTGTGAGAA
 TTTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATTCT
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT
 55 CTCATTTTACACACCAATGTACTTCTTCTGGGCAACCTCTCTTTCCTGGATATCTGCTAT
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGTCAATGGGGTCAACAGAATGTCTGCT
TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC
ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA
ATTCAGCTGTGCAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA
5 TCATTTTCGCATGTGAAATATTAGCTGTCCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA
TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTCATTTTTTTC
TCCTATATGTTTCATCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG
CATTTTCCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT
ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC
10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT
GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAACCAATTCATA
A (SEQ ID NO: 362)

AOLFR196 sequences:

15 MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLVYTLTMVGNILLIILVNINSSLQIPMYFSLNL
SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFFAFADAECILILAAMAYDRYAAICNPLL
YTTLMSRRVCVFIVLAYFSGSTTSLVHVCLTFRLSFCGSNIVNHFFCDIPPLLALSCTDTQINQL
LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS
20 YSLDSDKVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ
ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC
TACCTCTCAGAGTCACACTGTTCTTGGTATTCTTCTGGTATATACATTAACATGGTCGGA
AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTCAAATTCCCATGTATTATTT
25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAAATGCTGG
CAAACCTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT
CTTCGCTTCTTTTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG
CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT
CATTTGTGTTGGCATATTTCACTGGAAGTACAACATCACTGGTCCATGTGTGCCTCACATTC
30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCACCTCTTCT
GGCTTTATCATGTACAGACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCAGCTTCA
TCCAGACCAGCACTTTTGTGGTAATATTTTCTTACTTCTGCATCCTCATCACTGTGTTG
AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG
CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCCACCACTAGCTATTCC
35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA
TAATTTATAGTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA
TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAGAATAGTCAATATCTAA (SEQ ID NO:
364)

AOLFR197 sequences:

40 MCYLSQLCLSLGEHTLHMGVMVRHTNESNLAGFILLGFSDDYPQLQKVLFLVILILYLLTILGNTTI
ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMKTIAYGGCLVHLYNSHALGS
TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCLMALASMAWLSGIATTLVQSTLTLQLPFCGH
RQVDHFICEVPVLIKLACVGTTFNEAELFVASILFLIVPVSFILVSSGYIAHAVLRIKSATRRQKAF
45 GTCFSLTLVVTIFYGTIIFMYLQPAKSRSRDQGKFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK
VLAKALGVNIL (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG
TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTCTGATTATCC
50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA
ATACCACCATCATTCTGGTTTCTCGTCTGGAACCCAAGCTTCATATGCCGATGTATTTCTTC
CTTTCTCATCTCTCCTTCCCTGTACCGCTGCTTCACCAGCAGTGTTATTTCCCAGCTCCTGGT
AAACCTGTGGGAACCCATGAAAACATATCGCCTATGGTGGCTGTTTGGTTCACCTTTACAAC
TCCCATGCCCTGGGATCCACTGAGTGCCTCCTTGGCTCTGATGTCCTGTGACCGCTATGT
55 GGCTGTCTGCCGTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG
CATCTATGGCATGGCTCAGTGGAATAGCCACCACCCTGGTACAGTCCACCCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC
AAGCTGGCTTGTGTGGGCACCACGTTTAAACGAGGCTGAGCTTTTGTGGCTAGTATCCTTT
TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAGTGTTG
AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTCCGGACCTGCTTCTCCACCTGACA
5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT
CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC
TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA
GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**
MENCTEVTKFILLGLTSVPELQIPLFILFTFIYLLTLCGNLGMMLLILMDSCLHTPMYFFLSNLSL
VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAYDRYAACVCKP
LHYTTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH
TSEVILVFMSSFNIFVLLVIFISYLFIFITILKMHSAGHQAALSTCASHFTAVSVFYGTIVIFIYLO
15 PSSSHSMDTDKMASVFYAMIIPMLNPVVYSLRNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC
TACAGATCCCCCTCTTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG
GGGATGATGTGCTGATCTGATGGACTTGTGTCTCCACACCCCCATGTACTTTTCTCCTCAG
20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTCATGGCTGGG
TTCCTTAGAGGAGACAAGGTCATCTCCTACAATGCATGTGCTGTTTCAGATGTTCTTCTTTGT
AGCCTTGGCCACGGTGGAAAATTACTTGTGGCCTCAATGGCCTATGACCGCTATGCAGCA
GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC
TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCAGTCTC
25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTCTGTGATGTTCCAGCAGTCATGGCTCT
GTCTTGTCTGTATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT
TTTTGTCTTCTAGTTATCTTTATCTCCTACTTGTTTCATATTCATCACCATCTTGAAGATGC
ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC
CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCCAGCTCCAGCCACTCCATGGAC
30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCTGTGGTCT
ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTTGAGAAGGCAAAAAT
TTCTATAA (SEQ ID NO: 368)

AOLFR199 sequences:
35 MDTGNKTL PQDFLLGFPQSQT LQLSLF MLFLVMYILT VSGNVAILMLVSTSHQLHTPMYFFLS
NLSFLEIWYTAAV PKALAILLGRSQTISFTSCLLQMYFV FSLGCTEYFLLAAMAYDRCLAICY P
LHYGAIMSSLLSAQLALG SWVCGFVAIAVPTALISGLSFCGPRAINHHFFCDIAPWIALACTNTQA
VELVAFVIAVVILSSCLITFVS YVYIISTILRIPSA SGRSKAFSTCSSHLTVVLIWYGSTVFLHVR
TSIKDALDLIKAVHVLNTV VTPVLNPFYITLRNKEVRETLLKKWK GK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAAC TCTGCCCCAGGACTTTCTCTTACTGGGCTTTCCTGGTTCTC
AAACTCTTCAGCTCTCTCTCTTTATGCTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT
AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCCATGTACTTCTT
TCTGAGCAACCTCTCCTTCTGGAGATTGGTATACCACAGCAGCAGTGCCCAAAGCACTG
45 GCCATCCTACTGGGGAGAAAGTCAGACCATATCATTTACAAGCTGTCTTTTGAGATGTACT
TTGTTTTCTCATTAGGCTGCACAGAGTACTTCCTCCTGGCAGCCATGGCTTATGACCGCTGT
CTTGCCATCTGCTATCCTTTACACTACGGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC
TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG
TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA
50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT
GGTTATCCTGAGTTCATGCCTCATCACCTTTGTCTCCTATGTGTACATCATCAGCACCATCC
TCAGGATCCCCTCTGCCAGTGGCCGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC
CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCCTTCACGTCCGCACCTCTATCAAAGAT
GCCTTGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTAAACC
55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG
GAAAATAA (SEQ ID NO: 370)

AOLFR200 sequences:

MTRKNYTSLTEFVLLGLADTLELQIILFLFFLVYITLTVLGNLGMILLIRIDSQ LHTPMYFFLANL
SFVDVCNSTTITPKMLADLLSEKKTISFAGCFLOMYFFISLATTECILFGLMAYDRYAAICRPLL
5 YSLIMSRTVYLKMAAGAFAGLLNFMVNTSHVSSLSFCDSNVIHHFFCDSPPLFKLSCSDTILKE
SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHAFSTCASHLTAILFYATCIYTYLRPSS
SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

10 ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC
TGGAGCTACAGATTATCCTCTTTTGTGTTTTCTTGATTTATACACTTACAGTACTGGGA
AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT
CCTGGCTAACCTGTCTTTGTGGACGTTTGTAACCACTACCATCACCCCAAAGATGCTG
GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTGCTGGCTGCTTCTACAGATGTACT
TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA
15 TGGCAGCCCATATGTCGCCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA
ATGGCAGCCGGGGCTTTTGTGTCAGGGTGTGCTGAACCTCATGGTCAACACAAGCCATGTCA
GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCCACTT
TTCAAGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG
TGAATATTGTGGGGACTCTGCTTGTGTCATCCTCTCCTCCTACTCCTACGTTCTCTTCTCCATT
20 TTTTCTATGCATTGCGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA
CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGCTAC
TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGATTCCCATGTTGAATC
CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA
GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

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AOLFR201 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTIPSTLVSLSERKTISLSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQSVFVQLPFCRNININHTCEILAVMKLACADISDN
30 EFIMLVATTLFILTPLLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIFYGTILFMYMKPKS
KETLNSDDLDATDKIISMFYGVMTMPMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:
373)

35 ATGGAATGGGAAAACCACACCATTTCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTAGAAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
CGGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT
40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTGTTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTGGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT
TGTTTCATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTGTGAGCATC
45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCCTCTACCTGTTACGCCCATCTGA
CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA
GACACTTAATTCGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA
GTAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

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AOLFR202 sequences:

MEWENHTILVEFFLKGLSGHPRLELLFFVLIFIMYVILLGNGTLILISILDPHLHTPMYFFLGNL
SFLDICYTTTIPSTLVSLSERKTISLSGCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR
YPIIMSKDAYVPMAAGSWIIGAVNSAVQTVFVQLPFCRNININHTCEILAVMKLACADISGN
55 EFILLVTTTLFLLTPLLLIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDA TDKLIFFYRVMT PMMNPLIYSLRNKDVKEAVKHLLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACCAACCATCTGGTGAATTTTTCTGAAGGGACTTTCTGGTCACC
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG
AATGGTACTCTCATTTTAATCAGCATCTTGACCCTCACCTTCACACCCCTATGTACTTCTT
TCTGGGGAACCTCTCCTTCTTGACATCTGCTACACCACCACCTCTATTCCCTCCACGCTAG
TGAGCTTCCTTTCAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT
CAGCTTGCCATGGGGACAACAGAGTGTGTCTTCTGGGCGTGATGGCCTTTGACCGCTAT
10 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTGTGGT
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT
TGTTCTTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC
15 TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCCTCTACCTGCTCAGCTCGTCTGA
CTGTGGTGATAACATTCTGTGGGACCATCTTCCTCATGTACATGAAGCCCAAGTCTCAAGA
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTCATATTCTACAGGGTG
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA
GTAAACACCTACTGAGAAGAAAAAATTTTAAACAAGTAA (SEQ ID NO: 376)

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AOLFR203 sequences:

MKRQNQSCVVEFILLGFSNPELQVQLFGVFLVIYVVTLMGNAITVIISLNQSLHVP MYLFLLN
LSVVEVSFSAVITPEMLVVLSTEKTMISFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLCETPPVLELVCADTFLF
25 EIYAFTGTILIVMVPFLILLSYIRVLFILKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKR TLIKLWRRKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT
GGTGGTGCTCTCTACTGAGAAAATATGATTTCTTTTGTGGGCTGTTTTGCACAGATGTAT
TTCATCCTTCTTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT
TGCTGCAATTTGCCATCCTCTGAACTACCCAGTGATTATGAACAGAGGGGTTTTTATGAAA
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCGGTA
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTGAAATCTATGCCTTCACAGGCACCATTTT
GATTGTTATGGTTCTTCTTGTGTGATCCTCTTGTCTTACATTGAGTTCTGTTTGCCATCCT
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCTCTCACCTCACA
40 TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45 **AOLFR204 sequences:**

MEKKKNVTEFILGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL
IDTVYSSSSAPKLIVDSFQEKKIISFNGCMAQAYAEHIFGATEIILLTVMACDCYVAICKPLNYTT
IMSHSLCILLVAVAVWVGFLHATIQLFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDHTLGLFV
AVNSGFICLLNFLILVVSYVILRSLKNSLEGRCKALSTCISHIIVVVLFFVPCIFVYLRSVTTLPI
50 DKAVAVFYTMVVPMLNPVVYTLRNAEVKSAIRKLWRKKVTS DND (SEQ ID NO: 379)

ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCAT
ATGGAGAAAGTCACGTTTGTAGTATTTTGGTTCTTTACATGATAACACTTTCAGGCAACC
TGCTCATTTGTGGTTACCATTACCACCAGCCAGGCTCTGAGCTCCCCCATGTACTTCTTCTG
55 ACCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTTCTCAGCTCCTAAGTTGATTGTGGA
TTCTTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIIFDSLHTPMYFFLCN
LSFLDVCYTSSSVPLILASFLAVKKKVSFSGCMVQMFI SFAMGATECMILGTMALDRYVAICYP
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFSTCSAHLTVVIIIFYGTIFFMYAKP
10 ESKASVDSGNEDIIEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDBGK (SEQ ID
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTCTCCTGGTAGGGCTTTCTGCCCACC
CAAAGCTCCAGACAGTTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGA
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCCATGATTTTCTT
CCTCTGTAATCTTTCTTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATTCTTG
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTTCTCTGGGTGTATGGTGCAAATGTTTAT
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT
GTGGCCATCTGTACCCACTGAGATACCCTGTCATCATGAGCAAGGGTGCCTATGTGGCCA
20 TGGCAGCTGGGTCCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT
GCAGTTACCATTCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCTGAATCTGAT
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATAATTTATTGTTGCCACTATTCT
GAGGATTCCTTCCACTGAAGGAAAACATAAGGCCTTCTCCACCTGCTCAGCCCACCTGACA
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT
CTGTTGATTCAGGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC
AAAAACATACTGTGTAGGAAAAAATTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILD SHLHTPMYLFSLNL
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP
LRYPVIMNRRTCVCQIAAGSWMTGCLTAMVEMMSVLP LSLCGNSIINHFTCEILAILKLVCVDT S
LVQLIMLVISVLLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFYGTALSMH
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFN TAFISILK (SEQ
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCCTGGGATTTTTTCACTACCC
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC
40 AACATTTTCTGATCTCCATCACCATTCTAGATTCCCACCTGCACACCCCTATGTACCTCTT
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG
CAAAC TTTGTTTCAGGGAGAAACACTATTTCAATTCTCAGGGTGCGCCACTCAGATGTACCT
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT
GTGGCCATCTGCAACCCCTGAGATACCCTGTCATCATGAATAGGAGAACCTGTGTGCAGA
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAATGATGTCTGTGCT
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTCACTTGTGAAATTCTGGCCATCT
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAGTTAATCATGCTGGTGATCAGTGACT
TCTTCTCCCCATGCCAATGCTACTCATTGTATCTCTTATGCATTTATCCTCGCCAGTATCC
TGAGAATCAGCTCAGTGGAAGGTCGAAGTAAAGCCTTTTCAACGTGCACAGCCCACCTGA
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATTGCTGATTA
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

AOLFR209 sequences:

MDKINQTFVREFILLGLSGYPKLEIIFLILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNLS
FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLLGMAFDTRYVAICNPLRY
5 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV
TLAVSNIAFLVPLLVIFFSYMFILYTI LR TNSATGRHKAFSTCSAHLTVVIIIFYGTIFFMYAKPKS
QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:
389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC
CCAAACTTGAGATCATTTTCTTTGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC
AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT
CCTGGGCAACCTCTCTTCTGGATATCTGCTATACAACCTCCTCCATTCCCTCAACACTGG
TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCAGATGTTCTT
15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCTCTGGCATGATGGCATTGTATCGTTAT
GTGGCCATCTGTAACCTCTGAGATACCCCATCATCATGAACAAGGTGGTGTATGTACTGC
TGACTTCTGTATCATGGCTTTCTGGTGGAATCAATTCAACTGTGCAAACATCACTTGCCAT
GCGATGGCCTTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC
TAAAATTAGCTTGTTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAATATTGCT
20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG
CGAACGAACCTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG
TGGTGATCATATTTTATGGTACCATCTTCTTTATGTATGCAAAACCTAAGTCCCAGGACCTC
CTTGGGAAAAGACAACCTTGCAAGCTACAGAGGGGCTTGTTTCCATGTTTTATGGGGTTGTGA
CCCCCATGTTAAACCCCATATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA
25 ATATTTGCTGAGCAGGAAAGCTATTAACCGTAA (SEQ ID NO: 390)

AOLFR210 sequences:

MMGRRNDTNVADFILTGLSDSEEVQMALFMLFLLIY LITMLGNVGMILLIIRLDLQLHTPMYFFL
THLSFIDLSYSTVVPKTLANLLTSNYISFTGCFAQMFCFVFLGTAECYLLSSMAYDRYAAICSP
30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSM SRLHFCD SNIIHHFFCDTSPILALSCTDTDN
TEMLIFIIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGT MIFTY LKPR
RKSYS LGRDQVAPVYFYTIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC
TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT
GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT
TTTTCTCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTACACCTAAAAC
CTTAGCGAACTTACTGACTTCCAACATATTTCTTTCACGGGCTGCTTTGCCCAGATGTTCT
GTTTTGTCTTCTTGGGTA CTGCTGAATGTTATCTTCTCTCCTCAATGGCCTATGATCGCTAT
40 GCAGCGATCTGCAGTCCCTTACACTACACAGTTATTATGCCCAAAAGGCTCTGCCTCGCTC
TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC
AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT
AGCTCTGTCTGCATGACACAGACAACATGCTGAAATGCTGATATTCATTATCGTGGTTCC
ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCT
45 GAAAATTAATTCCA CTTCAGGAAAGCAGAAAGCTTCTCTACTTGCGTCTCTCATCTCTTG
GGAGTCACCATCTTCTATGGA ACTATGATTTTTACTTACTTAAAGCCAAGAAAGTCTTATT
CCTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC
ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG
AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

AOLFR211 sequences:

MMGRRNNTNVADFILMGLTLSEEIQMALFMLFLLIY LITMLGNVGMILLIIRLDLQLHTPMYFFL
THLSFIDLSYSTVVPKTLANLLTSNYISFTGCFAQMFFAFLGTAECYLLSSMAHDRYAAICSP
LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSM SRLHFYDSNVIHHFFCDTSPILALSCTDTYNT
55 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTY LKPRK
SYS LGRDQVASVYFYTIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)

5 ATGATGGGTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG
 GGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATT
 10 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAAACC
 TTAGCGAACTTACTGACTTCCAACATATATTTCTTTACGGGCTGCTTTGCCAGATGTTCTT
 TTTGCCCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG
 CAGCGATCTGCAGTCCTCTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA
 15 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA
 GCTCTGTCTGCACTGATACATAACAACACCGAAATCCTGATATTCATTATTGTTGGTTCCAC
 CCTGATGGTGTCCCTTTTCACAATATCTGCATCCTATGTGTTTCTCTTTACCATCCTGA
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCCTCTCTCATCTCTTGGG
 AGTCACCATCTTTTATAGCACTCTGATTTTTACTTATTTAAACCAAGAAAGTCTTATTCCT
 20 TGGGAAGAGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCGTGCTGAATCCACT
 CATTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

AOLFR212 sequences:

20 MAGNNFTEVTVFILSGFANHPELQVSLFLMFLFIYLFVVLGNLGLITLIRMDSQLHTPMYFFLSN
 LAFIDIFYSSVTPKALVNFQSNRRSISFVGCFFVQMYFFVGLVCCECFLLGSMAYNRYIAICNPL
 LYSVVMSSQKVSNNWLGVMPIYVIGFTSSLISVWVISSLAFCDSINHFCDTALLALSCVDFTFGT
 EMVSFVLGFTLLSLLIITVYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD
 25 NTSSLTQAQVASVFYITIVIPMLNPLIYSLRNKDVKNALLRVIHRKLFP (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTGCAAATCACC
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCATTTATCTATTCACTGTTTTGGGA
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT
 30 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG
 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTTCTGGGATCAATGGCCTACAATCGCTACA
 TAGCAATCTGCAATCCCTTACTGTATTCAAGTAGTCATGTCCCAAAAAGTGTCCAATGGCT
 GGGAGTAATGCCATATGTGATAGGCTTCAAGCTCGCTGATATCTGTCTGGGTGATAAGC
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTGTGACACCACAGCTCTTTTAGC
 35 ACTCTCCTGTGTAGATACATTCCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACTTATATCATCATCATCTCAGCCATCCTGAG
 GATCCAGTCAGCAGCAGGCAGGCAGAAGGCCCTTCTCCACCTGCGCATCCCACCTCATGGCT
 GTAACATCTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCATTCCCATGCTGAATCCACTC
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA
 CTTTTTCCATGA (SEQ ID NO: 396)

AOLFR213 sequences:

45 MNSLGKLVSMILSAHVFCYSKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDBPRL
 EAVLFVFLFFYLLTLVGNFTIIISYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK
 TITYGGCVAQLYISLALGSTECILLADMALDRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA
 SSLIHATFTLQLPLCGNHRDLHFICEVPALLKLACVDTTVNELVLFVSVLVFVIPPALISISYGF
 50 TQAVLRIKSVEARHKAFSTCSSHLTVVIIFYGTIIYVYLQPSDSYAQDQGKFISLFYTMVPTLNP
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA
 ATTTAATTGTTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG
 ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTATCCTTCTAGGCTTCTCAGACCACC
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCCTTTTCTTCTACCTCCTGACCTTGTGGGA
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTTCATACCCCAATGTACTTTT
 TCTCAGCAACCTCTCTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCATTTTATTTGCGAAGTACCAGCTCTTCT
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTTTGTGTAGTGTTCTGT
 TTGTTGTCATTCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAACTTCTCTCGGGA
 AAATTGTGA (SEQ ID NO: 398)

AOLFR214 sequences:

15 MDKSNSSVVSEFVLLGLCSSQKLQLFYFCFFSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY
 YVVIMSRRTCTVLVMISWAVSLVHTLSQLSFTVNLPFCGPNVVDSSFCDLPRVTKLACLDSEYIIE
 ILIVVNSGILSLSTFSLLVSSYIILVTVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS
 20 PLDKFLAIFYTVFTPVLNPIIYTLRNRDMKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTACTGTTGGGACTCTGTAGTTCTC
 AAAAAGTCCAGCTTTTCTATTTTGTCTTCTCTGTGTGTATACAGTCATTGTGCTGGGA
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCCTATGTACTTTCT
 25 CTTGGGAAACCTTTCTTTGTTGACATTTGTCTAGGCTTCTTTTGTACCCCTAAAATGATTG
 CAGATTTTCTGAGTGCACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTCTTT
 ATTCACCTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAGCCAGTTATCATTTACTGTG
 30 AACCTGCCTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTGTGATCTTCTCGAGTCAC
 CAAACTTGCCTGCCTGGACTCTTACATCATTTGAAATACTAATTGTGGTCAATAGTGAATT
 CTTTCCCTAAGCACTTTCTCTCTCTTGGTCAGCTCCTACATCATTATTCTTGTACAGTTTG
 GCTCAAGTCTTCACTGCAATGGCAAAGGCATTTTCTACGCTGGCTTCCCATATTGCAGTA
 GTAATATTATTCTTTGGACCTTGCATCTTCTATGTGTGGCCCTTACCATCTCTCCTTT
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTCACCCCCGTCCTAAACCCCATTTTATA
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:
 400)

AOLFR215 sequences:

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNSPMYFLLSNL
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMLLVAMAYDRFIAICKPLH
 YSTIMNRRLCVIFVSISWAVGVLSVSHLAFTVDLPFCGPNEVDSSFCDLPLVIELACMDTYEM
 EIMTLTNSGLISLSCFLALIISYIILIGVRCRSSGSSKALSTLTAHITVVILFFGPCIFYWPF SRL
 45 PVDKFLSVFYTVCTPLNPIIYSLRNEDVKAAMWKLRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC
 AATGTCTTAATTATTGTCATTATTTCTTTGACTCCCATTTGAACTCTCCTATGTACTTCTTG
 50 CTCAGTAATCTTTCTTTTATTGATATCTGTCTAGTCTAATTTGCCACCCCCAAGATGCTTGT
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCCAGATATTCGTT
 CTTACAGTTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCACTCTGTGAGCCACTTGGCTTTTACAGTGG
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTTGTGACCTTCCCTTGGTGATA
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCCG
ATGCAGGTCTCCAGTGGGTCACTAAAGGCTCTTTCTACATTAACTGCCACATCACAGTG
GTCATTCTTTCTTCGGGCCTTGCAATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT
GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTGAAACCCCATCATCTACT
5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT
CCTGGAAAACTAG (SEQ ID NO: 402)

AOLFR216 sequences:

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL
10 TNLSIIDMSLASFATPKMITDYLTHGKTIISFDGCLTQIFFLHLFTGTEIILLMAMSFDRYIAICKPL
HYASVISPQVCVALVVASWIMGVMHMSMSQVIFALTLPCGPPYEVDSEFFCDLPVVFQLACVDTY
VLGLFMISTSGHIALSCFIVLFNSYVIVLVTVKHHSSRGSSKALSTCTAHFIVVFLFFGPCIFIYMW
PLSSFLTDKILSVFYTIPTPLNPIIYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT
GGGAACTACAGATGTTTTCTTTATGGTGTTTTCATTGCTTTATGTGGCAACAATGGTGGG
TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC
TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTTCGCCACCCCAAGATGATT
ACAGATTACCTAACAGGTACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT
20 TTCTCCACCTTTTCACTGGAAGTACAAACCATCTCTTTTGATGGCTGCCTTGTATAGGTAT
ATTGCAATATGCAAGCCCCCTGCACTATGCTTCTGTCAATAGTCCCCAGGTGTGTGTTGCTCT
CGTGGTGGCTTCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC
ACGTTACCATTCTGTGGTCCCTATGAGGTAGACAGCTTTTTCTGTGACCTTCTGTGGTGT
CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA
25 ATTGCGTTGTCTCTGTTTTATTGTTTTATTTAATTCATATGTTATTGTCTGTTACTGTGAA
GCATCATTCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTCATTGTTG
TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA
GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC
TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAACTGAAAAATAGGTTTCTAAATTT
30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

AOLFR217 sequences:

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH
SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAISEFGCMTQMFFLHLLGGAIEVLLISMSFD
35 RYVAICKPLHYLTMSRRMCVGLVILSWIVGIFHALSQLAFTVNLPFCGPNEVDSEFFCDLPVIK
LACVDTYILGVFMISTSGMIALVCFILLVISYTIILVTVRQRSSGGSSKALSTCSAHFTVVTLFFGP
CTFIYVWPFTNFPIDKVLVSVFYTIYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP
(SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC
GAATTCATACTACGGGGTCTGTCCAGTCTTTAGAACTCCAGATTTTCTACTTCCTGTTTTT
CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTGCATCA
GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC
CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC
45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGCTGAGATTG
TACTGCTGATCTCCATGTCCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA
ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTTCTGGAATTGTCGGCATCT
TCCATGCTCTGAGTCAGTTAGCATTTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT
AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAAACTTGCTTGTGTGACACATATATTC
50 TGGGGGTGTTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCCTCTTGGT
GATCTCTTACACTATCATCCTGGTCACCGTTCCGGCAGCGTTCTCTGGTGGATCCTCCAAA
GCCCTCTCCACGTGCAGTGCCCACTTTACTGTTGTGACCCTTTTCTTTGGCCCATGCACTTT
CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA
TATACTCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC
55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA
(SEQ ID NO: 406)

AOLFR218 sequences:

METANYTKVTEFVLTLGLSQTREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA
LLDIWYSSITAPKMLIDFFVERKIIISFGGCIQLFHLFVGASEMFLIVMAYDRYAAICRPLHYA
5 TIMNRRLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTFPEELVM
ICSSGLISVVCFIALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVVLMFGPSIYIYARPD
SFSLDKVVSFHTVIFPLLNPIIYTLRNKEVKAAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC
10 GGGAGGTCCAACCTAGTCCTATTTGTIATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA
AATATCCTTATCATTGTCACCATCAGGCTAGACCCCTCATCTGACTTCTCCTATGTATTTCT
GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCATAAATGCTCA
TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT
CTTACACTTTGTTGGGGCTTCGGAGATGTTCTTGCTCATAGTGATGGCCTATGACCGCTAT
15 GCTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGTCTCTGCTGTATCCT
GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCATTCTATAATACAGGTGGCTCTCATTGTT
CGACTTCTTTCTGTGGGCCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG
TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT
GATCTCTGTGGTGTGTTTCATTGCTCTGTAAATGTCCTATGCCTTCTTCTGGCCTTGCTCA
20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACAT
TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT
TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCTTTACTTAATCCCAT
ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT
ATTTTGTGTGAAGAGAAGTGA (SEQ ID NO: 408).

25

AOLFR219 sequences:

MLTSLTDLFCSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLFLTFSLLYLAILLGNF
LIILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS
EMVLLVSMAYDRYVAICKPLHYMTVMSSRRVCVVLVLISWVFGFIHTTSQLAFTVNLPCGPN
30 KVDSFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVNRSSASMAKAR
STLTAHITVVTLFFGPCIFIYVWPFSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAAMSKLKS
RYLKPSQVSVVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAAGTATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT
35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG
TCTAGTTCAAGGGAGCTCCAACCTTTCTTGTTTCTTACATTTTCACTACTTTATCTAGCAAT
TCTGTTGGGCAACTTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA
TGTAATTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT
AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC
40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT
GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT
GTGTTGTGCTCGTCCTCATTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA
TTCACTGTTAATCTGCCATTTTGTGGTCTAATAAGGTAGACAGTTTTTTCTGTGACCTTCC
TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT
45 AGTGGCTTTCTTTCTCTGAGTTCTTTCTCCTCTGGTTGTCTCCTACACTGTAATACTTGTT
ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA
TCACTGTGGTCACTTTATTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT
TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCCTGT
AATCTACACGCTAAGAAACAAGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA
50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCTAGAAACAAAGTAA
(SEQ ID NO: 410).

AOLFR220 sequences:

MKQYSVGNQHSNYRSLFPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG
55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF
HSLGITESCVLTAIDAIDRYAICNPLRYPTIMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIIVILGMHSAEGHHKAFST
CAAHLAVFLFFGSVAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPIIYSLKNKDMKEAIGRLF
HYQKRAGWAGK (SEQ ID NO: 411).

5 ATGAAGCAATATTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTTGTTCCTTTTCT
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTCAATTGTCATCCAGGTGGGCATGGC
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCCTTCCTGGAGATCTGCTATACCA
10 CAACCACCATCCCCAAGATGCTGTCTGCTTAATCAGTGAGCAGAAGAGCATTTCGTTGGC
TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTG
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCCTCCTGTG
CTTCCTGAGATTGCATGGATTTCCACCTTGCTTTCTGTGGCTCCAACCAGATCCACCAGAT
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCCTGGTCAATTGCTCTATCCTACA
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAAGGCCTTTTC
CACCTGTGCTGCTCACCTTGCTGTGTTCTTGCTATTTTTTGGCAGTGTGGCTGTCATGTATT
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTTATC
20 CTTGCTCCCTTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:
412).

AOLFR221 sequences:

25 MRNLSGGHVEEFVLVGFPPTPPLQLLLFVLFFAIYLLTLENALIVFTIWLAPSLHRPMYFFLGH
LSFLELWYINVTIPRLLAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP
LLYPSLMPSSLATRLAAASWGSFGFSSMMKLLFISQLSYCGPNINHFFCDISPLLNLTCSDKEQA
ELVDLLALVMILLPLLAVVSSYTAIIAAILRIPTSRGRHKAFSTCAAHLAVVVIYSSTLFTYAR
PRAMYTFNHNKIISVLYTIIVPFFNPAIYCLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID
30 NO: 413).

ATGAGAAATTTGAGTGGAGGCCATGTCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC
CTCCCTCCAGCTGCTCCTCTTTGTCCTTTTTTTTGAATTTACCTTCTGACATTGTTGGAGA
ATGCACTTATTGTCTTCACAATATGGCTTGCTCCAAGCCTTCATCGTCCCATGTACTTTTTT
35 CTTGGCCATCTCTCTTTCCTGGAGCTATGGTACATCAATGTCACCATTCCTCGGCTCTTGGC
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACCTGACTTC
TTTATTGCCTGTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGTACCT
GGCCATCTGTGGACCCCTCCTTACCCTAGTCTCATGCCTTCCAGTCTGGCCACTCGCCTTG
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTTATTTCCTAA
40 TTGTCTACTGTGGACCCAACATTATCAACCCTTTTTCTGTGATATTTCCCACTACTCAA
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG
GTTGTTATCTACTACTCCTCCACTCTCTTACCTATGCACGGCCCCGGGCCATGTACACCTT
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT
GTCATATCCTAGGGATGTTTCAGGACTGA (SEQ ID NO: 414).

AOLFR222 sequences:

50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIIIAIRLDSHLHTPMYFLSFL
SFSETCYTLGIIPRMLSGLAGGDQAISYVGCAAQMFFSASWACTNCFLLAAMGFDRYVAICAPL
HYASHMNP TLCAQLVITSFLTGYLFGLMTLVIFHLSFCSSHEIQHFFCDTPPVLSLACGDTGPS
ELRIFILSLLVLLVSFFITISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIHYGCASFVYLRPK
ASYSLERDQLIAMTYTVVTPLLNPVYSLRTRAIQALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCCTCTCTGTATCTAGTCACTCTGACCAGC
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT
 CCTTTCCCTTCCATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT
 TTCTGCCTCATGGGCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT
 GGTCATTACTTCCTTCTGACTGGATACTCTTTGGACTGGGAATGACACTAGTTATTTTCC
 ACCTCTCATTTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG
 10 AGCCTAGCCTGTGGAGATACAGGCCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG
 TCCTCTTGGTCTCCTTCTTCTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG
 AGGATCCCCCTCTGCTGAGGGGCGAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG
 TGGTCATTATTCATTATGGCTGTGCTTCCTTCGTGTACCTGAGGCCCCAAAGCCAGCTACTCT
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA
 15 TTGTTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGGAG
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

AOLFR223 sequences:

MEAANESSEGISFVLLGLTTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA
 20 HLSFADLCFASVTVPKMLANLLAHDHSLAGCLTQMYFFFALGVTDSCLLAAMAYDCYVAIR
 HPLPYATRMSRAMCAALVGMALVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPLLRLSC
 SDTHHIQLLIFTEGA AVVTPFLLILASYGAIAAAVLQLPSASGRRLRAVSTCGSHLAVVSLFYGT
 VIAVYFQATSRREA EWGRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS
 (SEQ ID NO: 417).

25 ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTCGTTTTATTGGGACTGACAACAA
 GTCCTGGACAGCAGCGGCCTCTCTTTGTGCTGTTCTTGTCTTGTATGTGGCCAGCCTCCTG
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT
 TCCTGCTGGCCCCACCTGTCTTTGTGCTGACCTCTGTTTCGCCTCCGTCACTGTGCCAAGATG
 30 TTGGCCAACCTGTTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGGCTGACCCAAATGT
 ACTTCTTCTTTGCCCTGGGGTA ACTGATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG
 CTACGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGGCCATGTGCGCA
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCCACGTCCACTCCCTCCTGTATATCCTGCTCA
 TGGCTCGCTTGTCTTCTGTGCTTCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTCACCGAGGGCG
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCTCGCCTCCTATGGGGCCATCGCAGCTGC
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCCAC
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTGATGTACACTGTAGTCACCCCCATGC
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT
 CATTGGGCGAAGGATCTCAGCTAGTGACTCCTGA (SEQ ID NO: 418).

AOLFR224 sequences:

MGSFNSTFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTIIIALSWLDLRLHTPMYFFLSHL
 45 LDLCFTTSTVPQLLINLCGVDRITRGGCVAQLFIYLALGSTECVLLVVMADFDRYA AAVCRPLHY
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTCGSHLLVVFLFYGSAIYT
 YLQSIHNYSEREGKFVALFYTHITPILNPLIYTLRNDVKGALWKVLWRGRDSG (SEQ ID NO:
 419).

50 ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC
 CGCAACTGGAGCCCATCCTGTTTGTCTTATTTTTATTTTCTACTCCCTAACTCTCTTTGGC
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTCACCACCAGCACCGTGCCCCAGCTCCTGA
 55 TCAACCTTTGCGGGGTGGACCGCACCATACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGTATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCGTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT
GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACTCTCTGATCCAGACAGGTCTCGCAATG
GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA
5 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCGAGTCATAGT
CGTGGCTGTTCTGCAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG
AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA
GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC
TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATTCTCAATCCTC
10 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG
GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

AOLFR225 sequences:

MENYNQTSTDFILLGLFPPSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID
LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLIRM
15 SKRVCVLMITGSWIIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV
FLSATIFLVFPFIGISCSYGQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRPRS
LRSPTEKVLAVFYTILTPMLNPIIYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTCATCTTATTGGGGCTGTTTCCACCATCAA
20 TAATTGACCTTTTCTTCTTCATTCTCATTGTTTTCACTTTCTGATGGCTCTAATTGGAAACC
TGTCCATGATTCTTCTCATCTTCTTGACACCCATCTCCACACACCCATGTATTTCTACTG
AGTCAGCTCTCCCTCATTGACCTAAATTACATCTCCACCATTGTTCTAAGATGGCATCTGA
TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTGAGAGTTTCTTCTTCT
TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGC
25 TATTTGCTTTCCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA
ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA
TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT
CTGGCCTGCATGGACACCTGGGTCTATGAGGGCACAGTGTTTTTGAGTGCCACCATCTTTC
TCGTGTTTCCCTTCATTGGTATTTTCATGTTCTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC
30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCACCTCACTGTA
GTAACCTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC
AACAGAGGACAAGGTTCTGGCTGTCTTCTACACCATCCTCACCCCAATGCTCAACCCCATC
ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC
TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

AOLFR226 sequences:

MEWRNHSGRVSEFVLLGFPAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL
ANMSFLEIWYVTVTIPKMLAGFVGSQDHDGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD
RYMAICYPLHYPIVSVGRLCVQMAAGSWGAGGISMVKVFLISGLSYCGPNIINHFFCDVSPLL
40 NLSTDMSTAEFLTDFILAILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVIIIF
YAASIFIYARPKALSAFDTNKLVSVLVAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP
KKASRVN (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT
45 CCTGCGCCACTACAGGTACTATTGTTTGCCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC
TGAGAACACACTCATCATTATGGCAATTAGGAACCATCTACCCTCCACAAACCCATGTAC
TTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCACTGTCACTATTCCCAAGAT
GCTTGCTGGCTTTGTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC
ATGACACAGCTCTACTTTTTCTTGGCTTGGCTGCACTGAGTGTGTCCTTCTCGCTGTTAT
50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC
GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA
AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG
ATGTCTCTCCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTCT
ATCCTGGCCATTTTTATTCTTCTAGGGCCACTCTCTGTCACTGGGGCCTCCTATGTGGCCAT
55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT
GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA
CCATTGCTCAATCCCATCATTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCCTATGCT
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA
G (SEQ ID NO: 424).

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AOLFR227 sequences:

MEPQNTSTVTNFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVIITVVSQGLRLHSPMYMFLQH
LSFLEVWYTSTTVPLLLANLLSWGQAISFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP
LRYPFMLHRGLCARLVVVSWCTGVSTGFLHSMMSRLDFCGRNQINHFFCDLPPLMQLSCSRV
10 YITEVTIFILSI AVLICFFLTLPYVFIVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMIV
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTTCTCAGCTGTTAGGATTCCAGAACCTTC
15 TTGAATGGCAGGCCCTGCTCTTTGTCATTTTCTGCTCATCTACTGCCTGACCATTATAGGG
AATGTTGTATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT
TCCTCCAGCATCTCTCTTTCTGGAGGTCTGGTACACGTCCACCACTGTGCCCCCTTCTCCTA
GCCAACCTGCTGTCTGCGGCCAAGCCATCTCTTCTCTGCTGCATGGCACAGCTCTACT
TCTTCGTATTCCTCGGCGCCACCGAGTGCTTTCTCTGCGCTTCATGGCCTATGACCGTTAC
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT
GGTGGTGGTCTCATGGTGCACAGGGGTGAGCACAGGCTTTCTGCATTCCATGATGATTTC
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTCTTCTGCGACCTCCCGCCACTCA
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTATTGTGTCTCCATATT
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT
GTTGTCACTCTCTACTACGGGACCATGATCTCCATGTATGTGTGTCCAGTCCCCACCTGTT
GCCTGAAATCAACAAGATCATTCTGTCTTCTACACTGTGGTACACCACTGCTGAACCCA
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG
AAATGTGGTATTCTATGGAGTACAAGTAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

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AOLFR229 sequences:

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK
IILIHIDSR LHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAE
FFLLGLMSCDRYVAICNPLHYPDLMSRKICWLIVAAAWLGGSIDGFLTPVTMQPFCASREIN
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRRKAVAT
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQK
VVGRCVSSGKVTTT (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTTCCAACTTTATCATATCTCTTTTCGTGTACCCTACAGA
40 GCTATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTTCAGCA
ACGCCCCGTTTCCCCTGGCTTCTTTGCCCTCATTTCTCTGCTTTGTGACCTCCATAGCCAG
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCCATGTACTTC
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCT
GGTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTC
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCTCTAGGACTCATGTCCTGTGATCGCTA
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCGTCACCA
TGCAGTTCCCCTTCTGTGCTCTCGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT
CTGAAGCTCTCCTGCACGGACACATCAGCAGCAGACAGCCATGTATGTCTGTGCTATTAT
50 TGATGCTCCTCATCCCTTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT
CCTACTCATTACAGCCTTAGGAACAAGGATGTCACGGGGGCCCTACAGAAGGTTGTTGGG
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).

AOLFR230 sequences:

MGMEGLLQNSTNFVLTGLIHPAFPGLLFAIVFSIFVVAITANLVMILLIHMSRLHTPMYFLLS
QLSIMDTIYICITVPKMLQDLLSKDKTISFLGCAVQIFLYLTIGGEFFLLGLMAYDRYVAVCNP
LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSDTDS
5 LYETLMYACCVLMMLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSIFYGAIFY
TNVLPHSYHTPEKDKVVSIFYTILTPMLNPLIYSLRNKDVAALRKVLGRCGSSQSIRVATVIR
KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC
10 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA
GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCCTCCACACACCCATGTACTT
CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCCAAGATGC
TCCAGGACCTCCTGTCCAAGGACAAGACCATTCTCTTCTGCTGGGCTGTGCAGTTCAGATCTT
CCTCTACCTGACCCTGATTGGAGGGGAATTCTTCTGCTGGGTCTCATGGCCTATGACCGC
15 TATGTGGCTGTGTGCAACCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT
CATGGTGGTCGGCTCCTGGGTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT
ATGAGTTTCCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT
GCTGAAGTTGTCTTGCACAGACACGTCACCTCTATGAGACCCTGATGTATGCCTGCTGCGTG
CTGATGCTGCTTATCCCTCTATCTGTCTCTCTGTCTCCTACACGCACATCCTCCTGACTGT
20 CCACAGGATGAACTCTGCTGAGGGCCGGCGCAAAGCCTTTGCTACGTGTTCTCCCACATT
ATGGTGGTGAGCGTTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC
ACACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCCCATGCTCAA
CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG
GAGATGTGGTTCTCCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID
25 NO: 430).

AOLFR231 sequences:

MERANHSVVSEFILLGLSKSQNLQILFFLGFSVVFVGIVLGNLLILVTVTFDSSLHTPMYFLLSNL
SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMADRYVAICKP
30 LHYMTIMSPRVLTGLLLSSYAVGVFHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI
LQLLVIADSGLLSLVCFLLLLVSYGVIIFSVRYRAASRSSKAFSTLSAHITVVTLFFAPCVFIYVW
PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCACTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC
35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA
AACCTGCTCATCTTGGTGACTGTGACCTTTGATTTCGCTCCTTCACACACCAATGTATTTTCT
GCTTAGCAACCTCTCCTGCATTGATATGATCCTGGCTTCTTTTGCTACCCCTAAGATGATTG
TAGATTTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTCCCAGATGTTCTT
TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT
40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC
TACTGTTATCCTCCTATGCAGTTGGATTTGTGCACTCATCTAGTCAAATGGCTTTCATGTTG
ACTTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTCTGTGACCTTCCCCTTGTGAT
TAAACTTGCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC
CTGTCACTGGTCTGCTTCTCCTCTTGTCTCCTATGGAGTCATAATATTCTCAGTTAG
45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG
TGACTCTGTTCTTTGCTCCGTGTGTCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA
GATAAAATTCTTCTGTGTTTACACAATTTTACACCTCTCTTAAATCCTATTATTATAC
ATTAAGAAATCAAGAGGTAAGAGCAGCCATTAAGAAAGACTCTGCATATAA (SEQ ID NO:
432).

50

AOLFR232 sequences:

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV
VIFVFLMALSGNAVILLIHCD AHLHTPMYFFISQLSLMDMAYISVTVPKMLLDQVMGVNKIS
APECGMQMFFYVTLAGSEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD
55 GFTFTPITMTFPFRGSREIHHFFCEVPAVLNLSCSDTSLYEIFMYLCCVLMLLIPVVISSYLLILL

TIHGMNSAEGRKKAFATCSSHLTVVILFYGAAIYTYMLPSSYHTPEKDMMVSVFYTILTPVVPN
LIYSLRNKDVMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA
CTGTGACGCCCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA
TGGCGTACATTTCTGTCACTGTGCCAAGATGCTCCTGGACCAGGTTCATGGGTGTGAATAA
10 GATCTCAGCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA
TTTTCTCTTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA
CCCTGTCCTCATGAACCATAGGGTGTGTCTCTTCTGTCATCAGGCTGCTGGTTCCTGGGCT
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCTTCCGTGGATCCCGGGA
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCCTCATGCTCCTCATCCCTGTGGTGATCATT
TCAAGCTCCTATTTACTCATCCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA
AAAAGGCCTTTGCCACCTGCTCCTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC
ATCTACACCTACATGCTCCCCAGCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTG
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTAATCTATAGTCTTAGGAATAAGGAT
20 GTCATGGGGGCTCTGAAGAAAATGTAAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG
TAG (SEQ ID NO: 434).

AOLFR233 sequences:

25 MANITRMANHTGKLDFILMGLFRRSKHPALLSVVIFVVFLKALSGNAVLILLIHCD AHLHSPMY
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSDGFMLTPITMSFPFCRSWEIHFFCEVPAVTI
LSCSDTSLYETLMYLCCVLMLLIPVTIISSSYLLILLTVHRMNSAEGRKKAFATCSSHLTVVILFY
GAAVYTYMLPSSYHTPEKDMMVSVFYTILTPVLNPLIYSLRNKDVMGALKKMLTVRFVL
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAAG
GCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACTGTGACGCCCACCTCCACAGCC
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG
35 CCAAGATGCTCCTGGACCAGGTTCATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTCGGAATTTTTCTTCTAGCCACCATGGC
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCCTCATGAACCATAGG
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTCTCCTGGGCTCAGTGGATGGCTTCATGCTCAC
TCCCATCACCATGAGCTTCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG
40 TCCCTGCTGTAAACGATCCTGTCCTGCTCAGACACCTCACTCTATGAGACCCTCATGTACCTA
TGCTGTGTCCTCATGCTCCTCATCCCTGTGACGATCATTTCAGCTCCTATTTACTCATCCT
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGA AAAAAGGCCTTTGCCACCTGCTC
CTCCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC
45 GGTGCTGAACCCCTTAATCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA
ATGTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMLYLVTLMGNILIVTVTCDSSLHMPMYFFLRN
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFLTIMAHDRYVAVCQPL
HYPVIVNSRICIQMTLASLLSGLVYAGMHGTSTFQLPFCRSNVIHQFFCDIPSLKLSCSDTFSNE
VMIVVSALGVGGGCFIFIIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVSVFLSSCSSVYLRPP
AIPAATQDLILSGFYSIMPLFNPIIYSLRNKQIKVAIKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC
TACAGATTTTACATTCTGCATCCTTCTTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT
 CCCTACTGGACAGCACCACCATTTCTAAGGCGGGATGTGTAGCTCAGGTCTTCCTCGTGGT
 TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT
 GGCCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG
 CCCTTCTGTGCGGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT
 CTCTTGCTCTGACACCTTCAGCAATGAGGTGATGATTGTTGTCTCTGCTCTGGGGGTAGGT
 GGCGGCTGTTTCATCTTTATCATCAGGTCTTACATTACATCTTTTCGACCGGTGCTCGGGTT
 10 TCCAAGAGGAGCAGACAGAAACAAAGGCCTTTTCCACCTGCATCCCTCACATCCTGGTGGTG
 TCAGTCTTCCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC
 CCAGGATCTGATCCTTTCTGGTTTTTATTCCATAATGCCTCCCCTCTTTAACCTATTATTTA
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

AOLFR235 sequences:

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL
 SSLDLAFATSSVPQMLINLWPGKTISYGGCITQLYVFLWLGATECILLVMAFDYVAVCRPL
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL
 20 NQAVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVVFIFYGSASYGY
 LLPAKNSKQDQGFISLFYSLVTPMVNPLIYTLRNMEVKGALRRLLGKGREVG (SEQ ID NO:
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC
 25 CCCAGCTGGAGATGATCTTTTTATAGCCATCCTCTTCTCCTATTTGCTGACCCTACTTGGG
 AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTCGCTACTAGTTCAGTCCCCCAAATGCTGA
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT
 CTTCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCAAGCTCTGCTGGCTGC
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT
 GCAGCTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT
 GATCAAACCTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCATTGCTCAGGCAGT
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC
 AGCAAACAGGACCAGGGCAAGTTCATTCCCTGTTCTACTCGTTGGTACACCCATGGTGA
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

AOLFR236 sequences:

MTSQERDTAIYSINVSFVAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHLSFLDACLSTVTPKVMAGLLTLDGKVIS
 FEGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH
 45 AAIHTSLTFRLLYCGPCHIAFYFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA
 AVLIRTAQGRQRAFPCTAQLTGVLVYVPPVCIYLQPRSEAGAGAPAVFYTIVTPMLNPFYI
 TLRNKEVKHALQRLLCSSFRETAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA
 CTGTGGTGAGCCACTTCTTCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT
 CTTCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCCATGTACCACTTCTGGGGCACCTCTCCTTC
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTGATGGCAGGCCTGCTGACTCTGG
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC
 TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTCCGCCTGCTCTACT
 GTGGGCCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCCTGTCCTAAAGCTCGCCTGT
 ACAGACACCACCATTAAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT
 5 GCCTCATCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA
 GCCAGGGCCGCGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT
 ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC
 CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTACACTTTGCGGA
 ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTCCGAGAGTCTACAG
 10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

AOLFR237 sequences:

MDQRNYTRVKEFTFLGITQSRELSQVLFTFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL
 RNLSILDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFFHLLGGADVFSLSVMAFDRIYAISKPL
 15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLPLPVCGPVLDTFYCDVPQVLKLACTDTFT
 LELLMISNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIYVYA
 RPFTALPTDTAISVTFTVISPLLNPIIYTLRNQEMKLMRKLKRRLGQSERILIQ (SEQ ID NO:
 443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCTGGGAATTACTCAGTCCC
 GAGAACTGAGCCAGGTCTTATTTACCTTCTGTTTTTGGTGTACATGACAACCTCTAATGGG
 AAACTTCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC
 TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCTCTG
 ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT
 25 TCTTCCACCTTCTGGGGGGGAGCAGACGTTTTTCTCTCTGTGATGGCGTTTGACCGCTAT
 ATAGCCATCTCCAAGCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC
 TCATCGTGGGCTTCTGGGTGGGGGGCTTGTCCTCCATAGCGCAGATTTCTCTATTGCT
 CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTCTACTGCGATGTCCCCCAGGTCC
 TCAAACCTTGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT
 30 AGTCAGTTGGTTTGTATTCTTTCTCTCTCATATCTTACACGGTCATCTTGATGATGCTGA
 GGTCTCACCTGGGGAAGGAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG
 TGGTGACCTGCATTTTCGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCC
 ACAGACACTGCCATCTCTGTCACTTCACTGTCTATCTCCCTTTGCTCAATCTATAATTTA
 CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAAACTGAAGAGACGGCTAGGAC
 35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

AOLFR238 sequences:

MAPENFTRVTEFILTGVSSCPQLIPLFLVFLVLYVLTLMAGNLGIITLTSVDSRLQTPMYFFLRHL
 AIINLGNSTVIAPKMLMNLVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP
 40 LLYMVVVSRRLLCLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCIDIAPLLALSCSDTYIPE
 TIVFISAATNLFFSMITVLVSYFNIVLSILRIRSPEGRKKAFSTCASHMIAVTVFYGTMLFMYLQP
 QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:
 445).

45 ATGGCTCCTGAAAATTTACACAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC
 CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG
 GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCCATGTACTTTT
 TCCTGAGACATCTAGCTATCATCAATCTTGGCAACTCTACTGTCATTGCCCCATAAATGCTG
 ATGAACTTTTAGTAAAGAAGAAAACCTACCTCATTCTATGAATGTGCCACCCAACCTGGGAG
 50 GGTCTTGTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA
 TGTGGCCATTTGTAACCCTCTGCTCTACATGGTGGTGGTGTCTCGGCGGCTCTGCCTCCTGC
 TGGTGTCCCTCACGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTACCTTGTATATTC
 TCTGTGTCTATTGCTCTTCTAATAATCAATCATTTTTACTGTGATATTGCACCTCTGTT
 AGCATTATCTTGTCTGATACTTACATAACCAGAAACAATAGTCTTTATATCTGCAGCAACA
 55 AATTTGTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTGTCCATTCTA
 AGGATACGTTACACAGAAGGAAGGAAAAAGCCTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT
CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTATGCTGAATCC
CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT
CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

5

AOLFR239 sequences:

MDPQNYSLVSEFVLHGLCTSRHLQNFFIFFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG
NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCAQIFLHFTGGAEMVLLVSMAYDRYVAIC
KPLHYMTLMSWQTCIRLVLASWVVG FVHSISQVAFVNLPCGPNEVDSFFCDLPLVIKLACM
10 DTYVLGHMISDSGLLSLSCFLLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV
YVRPFSRFSVDKLLSVFYTIFTP LLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTCAGAAATTTGTGTTGCATGGACTCTGCACTTCAC
GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT
15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT
CCTGTGGGGAACCTAGCTTTCCTGGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG
ATCAGGGATTTCTTAGTGATCAAAAACTCATCTCCTTTGGAGGATGTATGGCTCAAATCT
TCTTCTTGCACTTTACTGGTGGGGCTGAGATGGTGCTCCTGGTTTCCATGGCCTATGACAG
ATATGTGGCCATATGCAAAACCCTTGCAATTACATGACTTTGATGAGTTGGCAGACTTGCACTC
20 AGGCTGGTGCTGGCTTCATGGGTGCTGGATTGTGCACTCCATCAGTCAAGTGGCTTTCA
CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG
GTGATCAAACCTTGCTGCAATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG
GGTTGCTTTCCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT
ATCAGACAGCGTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA
25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTTGTTTATGTGCGGCCTTTCAGTAGGTTT
TCTGTGGACAAGCTGCTGTCTGTGTTTTATACCATTTTACTCCACTCCTGAACCCCATAT
CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT
GACTTTTCAATGA (SEQ ID NO: 448).

30 **AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGPLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR
QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAQMYVFIVLGISECCLLTAMAYDRYVAIC
QPLRYSTLLSPRACLAMVGSSWLTGIITATTHASLIFSLPFRSHPIIPHFLCDILPVLRLASAGKHR
SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRKVFSTCSSHLLVVSFFGTASITYIRPQ
35 AGSSVTTDRVLSLFYTVITPMLNPIIYTLRNDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA
AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACTTGTCTGGG
40 TAACTCCCTGATCATCCTCCTCACACAGGTACAGCCTGCCCTGCACTCCCCCATGTACTTCT
TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCT
GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGCAGCCCAGATG
TACGTCTTCATTGTCTGGGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC
GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCCTCTTGAGCCCACGGGCTGCTT
GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC
45 ATCTTCTCTTACCTTTTCGACGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC
AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC
CATAGTCTTCATTATGATCCCCCTTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG
CCATCCTAGCAATGGCCTCCACCCAGAGCCGCCGCAAGGTCTTCTCCACCTGCTCCTCCCA
TCTGCTCGTGGTCTCTCTCTTTTGAACAGCCAGCATCACCTACATCCGGCCGCAGGCA
50 GGCTCCTCTGTTACCACAGACCGCGTCTCAGTCTCTTCTACACAGTCATCACACCCATGCT
CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT
GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

AOLFR241 sequences:

55 MPQILIFTYLNMFYFFPLQILAENLTMVTEFLLLG FSSLGEIQLALFVVFLFLYLVLSGNVTIIS
VIHLDKSLHTPMYFFLGILSTSETFYTFVILPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAACAIGGFLASLTVVNLVFSLPFCSANKVNH
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTILKIPSAEGRRKAFSTCAS
HLSVVIVHYGCASFIYLRPTANYVVSNDRLVTVTYITVTPLLNPMVYSLRNKDVQLAIRKVLG
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTTGCTGGGTTTTCCAGCCTTGGT
GAAATTACAGCTGGCCCTCTTTGTAGTTTTCTTTTCTGTATCTAGTCATTCTTAGTGCCAA
TGTCACCATTATCAGTGTTCATCCACCTGGATAAAAGCCTCCACACACCAATGTACTTCTTCC
10 TTGGCATTCTCTCAACATCTGAGACCTTCTACACCTTTGTCATTCTACCCAAGATGCTCATC
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT
CCTTGGTTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG
CCATTTGTCACCCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGGAAAACCTGGC
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTTCAGCC
15 TCCCTTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCAATTTGTGGAGTTCTTGTAC
TTGTGGTTCCTTTCTGTTTATCTGTGTTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG
ATTCCCTCAGCTGAGGGCAGACGGAAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTTG
TTATTGTTCAATTATGGCTGTGCTTCTTCATCTACCTGAGGCCTACAGCAAACCTATGTGTCC
20 AACAAAGACAGGCTGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTTGGGCAAGAAA
GGTTCTCTAAAACCTATATAATTGA (SEQ ID NO: 452).

AOLFR242 sequences:

25 MNTTLFHPYSFLLLIGIPGLESMLHWVGPFPAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESAVLVAMAYDCYVAICDPLCY
TLVLTNKVVSVMALAIPLRPLVFVIPFVLFILRLPFCGHQIIPHTYGEHMGARLSCASIRVNIYIG
LCAISILVFDIIAIVISYVQILCAVFLSSHDARLKAFSTCGSHVCVMLTFYMPAFFSFMTHFRGR
NIPFHIHILLANFYVVIPALNSVIYGVRTKQIRAQVLKMFENK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCCTTACTCTTTCTTCTTCTGGGAATTCCTGGGCTGGAAAG
TATGCATCTCTGGGTTGGTTTTCTTTCTTTGCTGTGTTCTCTGACAGCTGTCCTTGGGAATA
TCACCATCCTTTTTGTGATTACAGCTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTCTG
GCCATTCTGTCTATCTATTGACCCGGGCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCCAGATGTTCTTCTATCC
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC
CATCTGTGACCCCTTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTCAGTTATGGCA
CTGGCCATCTTTCTGAGACCCCTAGTCTTTGTGCATACCCCTTGTCTATTTATCCTAAGGCT
TCCATTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC
40 CTGTCTTGTGCCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT
CTTTGACATCATAGCAATTGTCAATTCCTATGTACAGATCCTTTGTGCTGTATTTCTACTCT
CTTCACATGATGCACGACTCAAGGCATTACAGCACCTGTGGCTCTCATGTGTGTGTCATGTT
GACTTTCTATATGCCTGCATTTTCTCATTATGACCCATAGGTTTGGTCGGAATATACCTC
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA
45 ATTTATGGTGTGAGAACCACAGATTAGAGCACAAAGTGCTGAAAATGTTTTCAATAAAT
AA (SEQ ID NO: 454).

AOLFR243 sequences:

50 MEQVNKTVVREFVVLGFSSLARLQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHTPMYFFLAIL
SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLLAAMGYDRYMAICNPLR
YSVLMGHGVCMLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLASQHSFG
SQLVIFMLGVFALVIPLLLILVSYIRIISAILKIPSSVGRYKTFSTCASHLIVVTVHYSCASFIYLRPK
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRITIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTGCTCCTCGGCTTCTCATCCCTGG
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTGCTCCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT
 CCTTGCCATCCTTTCTTGCTCTGAGATTTGCTATACCTTTGTCAATTGTACCCAAGATGCTGG
 TTGACCTGCTGTCCCAGAAGAAGACCATTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC
 TTCCTCTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGCTATGATCGCTATAT
 5 GGCCATCTGTAACCCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACTCCCTAGTATTTCA
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCTGTCTTA
 AACTGGCATCTCAGCACTCCGGCTTCAGTCAGCTGGTCATATTCATGCTTGGTGTATTTGC
 CTTGGTCATTCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA
 10 AAATCCCTTCCCTCCGTTGGAAGATAACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG
 GTAAGTGTACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC
 AAGCCAAGACACCCTAATATCTGTGTACATACCATCCTTACCCCATTTGTTCAATCCAATG
 ATTTATAGTCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAACT
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

AOLFR244 sequences:

MWQEYYFLNVFFPLLKVCLTINSHVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF
 MGLFNRKETSGLIFAIHSIIFFTALMANGVMIFLIQTDRLHTPMYFLLSHLSLIDMMYISTIVPKM
 LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLSRRVCWMI
 20 IAGSWFGGSLDGFLLPITMSFPFCNSREINHFFCEAPVLKLACADTALYETVMYVCCVLMML
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTVVSIFYGAAMYTYMLPHSYHKPAQ
 DKVLSVFYILTPLMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT
 TACCTTATATCGGCACAACCTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT
 CACTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT
 ATCATCTTCTTACCGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT
 TGCGCCTTCATACACCCATGTACTTCTCTCAGCCACCTTTCCTTAATTGACATGATGTAT
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCCTTCTCTG
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCTCTGAGATACCTGTCC
 TCATGAGCCGCGGGTCTGTTGGATGATTATAGCAGGTTCTGTTTGGGGGCTCTTTGGA
 TGGCTTCTCTAACCCTCATCACCATGAGCTTTCCTTCTGCAATTCCCGGGAGATTAAACC
 35 ACTTCTTCTGTGAGGCACCAGCAGTCCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTCTCTGTAGTCCTTGCTT
 CCTATGCCCCGAATCCTGACTACAGTTCAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG
 CATTTGCCACTTGCTCATCCCATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCCAGGACAAAGTCCTCTCTGTGTTTT
 40 ACACCATTCTCACACCCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCCTCAAAGGGTGTGAGGAGGTGT
 CTTTTGA (SEQ ID NO: 458).

AOLFR245 sequences:

MDLKNGLVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCRSTLHSPLYFLLGN
 45 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKP
 LHRYTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNVINNIFCDLPLVIKLACIETYTLE
 LFVIADSGLLSFTCFILLVSYIVILVSPVKSSHGLSKALSTLSAHIIIVTLFFGPCIFIYVWPFSSL
 ASNKT LAVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT
 GGGAACTTCAAATTTTCTTCTTTGTGACATTTTCCCTGATCTACGGTGCTACTGTGATGGGA
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCTTCATTCTCCCTTGACTTTCT
 CCTTGGAATCTCTCTTTTTTGGACATGTGTCTCTCACTGCCACAACACCCAAGATGATCA
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT
 CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG
TTTGCGATACTTTTCATGGATAATTGGTTTTTTTACACTCCATAAGCCAGATAGTTTTAACAAT
GAACCTGCCTTTCTGTGGCCACAATGTCATAAAACAACATATTTTGTGATCTTCCCTTGTGA
TCAAGCTTGCTTGCATTGAAACATACACCTTGAATTTTGTGATTGCTGACAGCGGGCT
5 GCTCTCTTTACCTGTTTCATCCTCTTGCTTGTCTTACATTGTCATCCTGGTCAGTGTACC
AAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCACATCATTGTG
GTCATCTGTTCTTTGGACCTTGATTTTTATCTATGTTTGGCCATTAGTAGTTTGGCAAG
CAATAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA
10 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT
CTGCACAGAATTTCTAG (SEQ ID NO: 460).

AOLFR246 sequences:

MSPENQSSVSEFLLGLPIRPEQQA VFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH
LALTDISFSSVTVPKMLMDMRTKYKSILYECCISQMYFFIFFTDLDSFLITSMAYDRYVAICHPL
15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLRLSFCANTIPHVFCDLAALLKLSCSDIFLNE
LVMFTVGVVITLPMFMCILVSYGYIGATILRVPSTKGIHKALSTCGSHLSVSVSLYYGSIFGQYLF
PTVSSSIDKDVIVALMYTVVTPMLNPFYSLRNRDMKEALGKLFSRATFFSW (SEQ ID NO:
461).

20 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC
CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGGGCATGTACCTGACCACGGTGCTGGG
GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTACCTTACACCCCCATGTACTTCT
TCCTCAGCCACTTGGCTCTCACTGACATCTCCTTTTTCATCTGTCACTGTCCCTAAGATGCTG
ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTTCTCAGATGTATT
25 TTTTATAATTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT
GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT
AGTGGCTGTATCTTGGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC
GGCTGTCTTTCTGTGCTGCGAACACCATCCCCCATGTCTTCTGTGACCTTGTGCCCCTGCTC
AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTACAGTAGGGGTGGTGG
30 TCATTACCCTGCCATTTCATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCCTCTG
AGGGTCCCTTCAACCAAAGGGATCCAAAGACATTTGTCCACATGTGGCTCCCATCTCTCTG
TGGTGTCTCTCTATTATGGGTCAATATTGTGCCAGTACCTTTTCCCGACTGTAAGCAGTTCT
ATTGACAAGGATGTGATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT
TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG
35 CAACATTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

AOLFR247 sequences:

MGQHNLTVLTEFILMELTRPELQIPLFGVFLVIYELITVVGNLTMILTKLDSHLHTPMYFSIRHL
ASVDLGNSTVICPKVLANFVDRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYVAICNPLL
40 YYVIMSQR LCHVLVG IQLYSTFQALMFTIKIFTLTFCGSNVISHFYCDDVPLLPMLCSNAQEIE
LLSILFSVFNLISSFLIVLVSYMLILLAICQMHSAGEGRKKAFTSTCGSHLTVVVVFYGSLLFMYMQ
PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTACAAGGCGGC
45 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC
AACCTAACTATGATCATTTTGACCAAACCTGGACTCCCACTTACATACACCTATGTACTTTTC
TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCATTTGTCCCAAGGTGCTGG
CAAATTTTGTGTGGATCGAAATACTATTTCTATTATGCATGTGCTGCACAGCTGGCATTCT
TTCCTTATGTTTCATTATCAGTGAATTTTTCATCCTGTCAGCCATGGCCTATGACCGCTATGT
50 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTCTCAGCGACTGTGTCATGTACTGG
TGGGCATTCAATATCTCTACAGCACATTTAGGCTCTGATGTTCACTATTAAGATTTTTACA
TTGACCTTCTGTGGCTCTAATGTCATCAGTCATTTTACTGTGATGATGTTCTTTGCTACC
TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT
TGATCTCCTCCTTTCTGATAGTCTTAGTGTCCTACATGTTGATTTTGTAGCTATATGTCAA
55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCCATTTGACAGTGG
TGGTTGTGTTCTATGGGTCTCTACTCTCATGTACATGCAGCCCAATTCCACTCACTTCTTT

GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTTGAT
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAATTGA
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPCALPTGGLLPHPQHTMMEIANVSSPEVFLVLLGFSTRPSLETVLFIVVLSFYMVLSILNGI
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL
ATECVLLATMSYDRIAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSSTLMLPLCG
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLPLGLILVSYGHIARAVLKIRSAEGR
10 RKAFTNCSSHVAVVSLFYGSIIIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTEVKS
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCCACAGGTGGCCTTTTGCCCCACCCCCAGCATACAAT
GATGGAAATAGCCAATGTGAGTTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA
15 CCCTCACTAGAACTGTCCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT
TTCTTGCCAACCTCCCTTCCTGGACATGAGCTTCACCACGAGCATTGTCCCACAGCTCCTG
GCTAACCTCTGGGGACCAAGAAAACATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCCTGTGCTGGCCACCATGTCCTATGACCGCT
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG
GCTAGCTTTGGCCTCCTGGCTGGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTTGCAGATGCCCCCTCA
TTATGCAACTGGCTTGTGTGGATACCAGCCTCAATGAGATGGAGATGTACCTGGCCAGCTT
TGCTTTTGTGTCTCTGCCTCTGGGGCTCATCTGGTCTCTTACGGCCACATTGCCCGGGCCG
25 TGTTGAAGATCAGGTCAGCAGAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCCACG
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

AOLFR249 sequences:

MKSQIEKSDLKYRAILLQKVTRMFLFWVLLLVLRLVVMGRGNSTEVTEFHLLGFGVQHEF
QHVLFIIVLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHILAFVDICYTSAITPKMLQSFTEN
NLITFRGCVIQLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQTVYIQLVAGSYIIGSI
35 NASVHTGFTFSLFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDLMFTELVIIFSIIYIM
VTILKMSSTAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAAGTGAAGTAAATATAGAGCCATTTTATTGCAAAAAGTC
40 ACAAGGATGTTCTGCTTTTCTGGGTCTTCTCTTGGTCCTTTCTAGACTTTTGGTAGTCAT
GGGTCGAGGAAACAGCACTGAAGTGAAGTGAATTCCATCTTCTGGGATTTGGTGTCCAACAC
GAATTTCAAGCATGTCCTTTTCACTGACTTCTTCTATCTATGTGACCTCCCTGATAGGAAA
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTC
CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTGGGGCTGTGTGATACAATTTCTAGTTT
ATGCAACATTTGCAACCAAGTGAAGTGTACCTCCTAGCTATTATGGCAATGGATTGTTATGT
TGCCATCTGTAAGCCCTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGGTCTCCCAATTCTTGC
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCCTGAAG
ATGCTTCTACTGCTGGGAGGAAAAATCCTTCTCCACATGTGCCTCCACCTGACAGCAG
TAACCATTTTCTATGGGACACTCTCTTACATGTACTTACAGCCTCAGTCTAATAATTCTCAG
GAGAATATGAAAGTAGCCTCTATATTTTATGGCACTGTTATCCCATGTTGAATCCTTTAAT
55 CTATAGCTTGAGAAATAAGGAAGGAAAAATAA (SEQ ID NO: 468).

AOLFR250 sequences:

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV
DMGLTSSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY
STVMRPQVCALMLALCWVLTNIVALHTHFLMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE
5 MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVVGKAFSTCSSHLVCVVFYGTLSAYLC
PPSIASEEKDIAAAAMYTIVTPMLNPFYISLRNKDMKGALKRFLSHRSIVSS (SEQ ID NO: 469).

ATGGA AAAACCAATCCAGCATTCTGAATTTTCTCCTCCGAGGAATATCAGCGCCTCCAGAGC
AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG
10 CTCATCATCCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC
CAACCTGTCTTTTGTGACATGGGTTTAACGTCCTCCACAGTTACCAAGATGCTGGTGAAT
ATACAGACTCGGCATCACACCATCTCCTATACGGGTGCCTCACGCAAAATGTATTTCTTTCT
GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC
ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC
15 ATTGTGCTGGGTCTCACCAATATCGTTGCCCTGACTCACACGTTCTCATGGCTCGGTTGT
CCTTCTGTGTGACTGGGGAATTTGCTCACTTTTCTGTGACATCACTCCTGTCTGAAGCTG
TCATGTTCTGACACCCACATCAACGAGATGATGGTTTTTGTCTTGGGAGGCACCGTACTCA
TCGTCCCCTTTTTATGCATTGTACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC
CGAACCCGTGGTGGGGTGGGCAAGGCCTTTTCCACCTGCAGTTCCACCTCTGCGTTGTTT
20 GTGTGTTCTATGGGACCCTCTTCAGTGCCTACCTGTGTCTCCTCCCTCCATTGCCTCTGAAGAG
AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT
ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA
TTGTTTCTCTTAG (SEQ ID NO: 470).

AOLFR251 sequences:

MEGNKTWITDITLPRFQVGPAL EILLCGLFSAFYTLTLLGNGVIFGIICLDCKLHTPMYFFLSHLA
IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVMSYDRYADICHPLRY
NILMSWRVCTVLAVASWVFSLLALVPLVLILRPFCEPHEINHFEILSVLKLACADTWNQV
VIFAACVFILVGPLCLVLVSYLRLAILRIQSGEGRRKAFSTCSSHLVCVGLFFGSAIVTYMAPK
30 SRHPPEEQQKVL SLFYSLFNPM LNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA
GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA
TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC
35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG
AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT
ATTTGGCTTTTGTCTACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG
GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCTGG
CTGTGGCTTCTGCGGTGTTTCTGCTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCTGAGG
40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCACTTCTGTGAAATCCTGTCTGTCTCAAGTT
GGCCTGTGCTGACACCTGGCTCAACCAGGTGGTTCATCTTTGCAGCCTGCGTGTTCATCCTG
GTGGGGCCACTCTGCCTGGTGTCTGCTCCTACTTGCATCCTGGCCGCCATCTTGAGGA
TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT
GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG
45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA
TATATAGCCTAAGGAATGCAGAGGTCAAGGGGCCCTGAGGAGGGCACTGAGGAAGGAG
AGGCTGACGTGA (SEQ ID NO: 472).

AOLFR252 sequences:

MRLANQTLGGDFLLGIFSQISHPGRLCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL
IDLTYISVTPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR
YSVLSHRVCLLLASGCWFVGSVDGFMLTPIAMSFPFCRSHEIQHFFCEVPAVLKLSGSDTSLY
KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSFLFYGAAIYNYML
PSSYQTPEKDMMSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAACCAGACCCTGGGTGGTGACTTTTTCTGTTGGAATCTTCAGCCAGA
 TCTCACACCCTGGCCGCCTCTGCTTATCTTCAGTATATTTTGTATGGCTGTGTCTTGG
 AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT
 TATAAACAGCTCTCACTCATAGACTTGACATATATTTCTGTCACTGTCCCCAAAATGCTG
 5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC
 TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT
 ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC
 CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA
 TGAGCTTCCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT
 10 TTGAAGCTCTCTTGTCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT
 CATGCTCCTGATACCTGTGACGGTCATTTCAAGTGTCTTACTACTATATCATCCTCACCATCC
 ATAAGATGAACTCAGTTGAGGGTCGAAAAAAGGCCTTCACCACCTGCTCCTCCACATTAC
 AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACCTACATGCTCCCCAGCTCCTACCAA
 ACTCCTGAGAAAGATATGATGTCATCCTTTTTCTACACTATCCTTACACCTGTCTTGAATCC
 15 TATCATTTACAGTTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAAATGCTGAGCGT
 GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

AOLFR253 sequences:

20 MTFFSSGGNCEPVMCSGNQTSQNQTASTDFLTGLFAESKHAALLYTVTFLLFLMALTGNALL
 ILLIHSEPR LHTPMYFFISQLALMDLMLCVTPKMLVGQVTGDDTISPSCGCIQMFFHLTLAG
 AEVFLLAAMAYDRYAAVCRPLHYPLLMNQRVCQLLVSAWVLMVDGLLLTPITMSFPFCQS
 RKILSFFCETPALLKLSCSDVSLYKMLTYLCCILMLLTPIMVISSSYTLHLIHRMNSAAGRKA
 LATCSSHMIIVLLFGASFYTYMLRSSYHTAEQDMMVSAFYTIFTPLNPLIYSLRNKDVTRAL
 RSMMQSRMNQEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT
 CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA
 TGCTGCCCTCCTCTACACCGTGACCTTCTTTCTTGTATGGCCCTCACTGGGAATGCCC
 30 TCCTCATCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCATGTACTTCTTCATCAGC
 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC
 AGGTCACTGGAGATGATACCAATTTCCCGTCAGGCTGTGGGATCCAGATGTTCTTCCACCT
 GACCTTGGCTGGAGCTGAGGTTTCTCCTGGCTGCCATGGCCTATGACCGATATGCTGCT
 GTTTCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT
 CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT
 35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC
 TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT
 CTCACCCCATCATGGTCATCTCCAGCTCATAACCCTCATCCTGCATCTCATCCACAGGAT
 GAATTCTGCCGCCGGCCGAGGAAGGCCTTGGCCACCTGCTCCTCCACATGATCATAGTG
 CTGCTGCTCTTCGGTGCTTCTTCTACACCTACATGCTCCGGAGTTCTACACACAGCTGA
 40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT
 ACAGTCTCCGCAACAAAGATGTCACCAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA
 ACCAAGAAAAGTAG (SEQ ID NO: 476).

AOLFR254 sequences:

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI
 MDTLFICTTVPKLLADMVSKEKHSFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP
 VLMNRKKCLLLAAGAWFGGSLDGFLLPITMNVPCGSRSSINHHFCEIPAVLKLACADTSLYET
 LMYICCVLMLLIPISIISTSYSLILLTIHRMPSAEGRKKAFTTCSHLTVVSIFYGAIFYTYVLPQS
 50 FHTPEQDKVVSIFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACCSSAQKVATSDA (SEQ ID NO:
 477).

55 ATGACGAACACATCATCCTCTGACTTCACCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG
 CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAATTTGGT
 CATGATATTCTTGATTGAGGTGGACTCTCGCCTCCACACCCCATGTACTTTCTGCTCAGTC
 AGCTGTCCATCATGGACACCCTTTTTCATCTGTACCACTGTCCCAAACTCCTGGCAGACAT
 GGTTTCTAAAGAGAAGATCATTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT
 CTGTAACCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGCTTTTGCTGGCTGCT
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC
 5 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT
 GGCCTGTGCAGACACGTCCTTGATGAAACTCTGATGTACATCTGCTGTGTCCTCATGTTG
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT
 GCCCTCTGCTGAAGGTCGCAAAAAGGCCTTCACCACTTGTCCTCCCACTTGACTGTAGT
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG
 10 AGCAGGACAAAGTAGTGTACGCCTTCTATACCATTGTACGCCCATGCTTAATCCTCTCAT
 CTACAGCCTCAGAAACAAGGACGTATAGGGGCATTTAAAAAGGTATTTGCATGTTGCTCA
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

AOLFR255 sequences:

15 MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSRHTPMYFLLSQLS
 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH
 YPVLMSRKICWLIVAAAWLGGSIDGFLLPVTMQPFCASREINHFFCEVPALLKLSCDTDSAY
 ETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEAEGRGKAVATCSSHMVVVSLFYGAAMYT
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTF (SEQ
 ID NO: 479).

20 ATGGAGCAGAGCAATTATTCGTTGATGCCGACTTTATCCTTCTGGGTTTGTTCAGCAACG
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTTGACCTCCATAGCCAGC
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCTCCACACCCCCATGTACTTCTT
 25 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCCACCATTGTGCCCAAAATGCTG
 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCTTTGCTGGATGCACTGCCCAACACTTCC
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCCTCCTAGGACTCATGTCCTATGATCGCTAC
 GTAGCCATCTGCAACCCTCTGCACTATCCTGTCTCATGAGCCGCAAGATCTGCTGGTTGA
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT
 GCAGTTCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT
 GATGTCCTCATCCCTTTCTCTGTCTATCTCGGGCTTTACACAAGAATTCTCATTACTGTTT
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG
 TGGTTGTACGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC
 ACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGGA
 GGTGTGTGCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

AOLFR256 sequences:

40 MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLGNGVIFGHIICLDSKLHTPMYFFLSHL
 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF
 QYTVIMSWRVCTILASTCWISFLMALVHITHILRPPFCGPQKINHFICQIMSVFKLACAGPRLNQ
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPVMGRAADRLTLPAPSHLCMVGLLFGSTMVM
 YMAPKSRHPEEQKVLSLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:
 481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAATTCATCCTGGTGGGATTCCAGGTTGGTCCA
 GCACTGGCGATTCTCCTCTGTGGACTCTTCTCTGTCTTCTATACACTCACCTGCTGGGGAA
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC
 50 TCTCACACCTGGCCATCATTGACATGTCCTATGCTTCCAACAATGTTCCCAAGATGTTGGC
 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG
 TATTTGGCTTTTGTGCTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT
 GGCCATCTGCCACCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG
 55 GCCGCTTTTGTGGCCCAAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCAT
 AATTGGCCTGTGCTGGCCCTAGGCTCAACCAGGTGGTCTATATGCGGGTTCTGCGTTCAT
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGGCCATCTT

5 GAGGATCCAGTAATGGGGAGGGCCGACACCGACTTACTCTTCCTGCTCCTTCCACCTTT
GCATGGTGGGACTCCTTTTTGGCAGCACCATGGTCATGTACATGGCCCCAAGTCCCGCCA
CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC
CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGGCCTGAAAAGAGTGTTGTGG
AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

AOLFR257 sequences:

10 MESNQTWITEVILLGFQVDPALELFLFGFFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL
AIVDMSYASSTVPMKLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMCYDRYVAICHPL
QYTLIMNWRVCTVLA STCWIFSLLALVHITLILRPF CGPQKINHFFCQIMSVFKLACADTRLN
QVVLFAGS AFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM
APKSSHSQERRKILSLFYSLFNPI LNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

15 ATGGAAGCAATCAGACCTGGATCACAGAAGTCATCCTGTTGGGATTCCAGGTGGACCCA
GCTCTGGAGTTGTTCTCTTTGGGTTTTCTTGCTATTCTACAGCTTAACCCTGATGGGAAA
TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC
CTGTCACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG
CAAACTTGTGATGCACAAAAAGTCATCTCCTTTGCTCCTTG CATACTTCAGACTTTTTTG
TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG
20 TGGCAATCTGTCAACCCCTTGAATACACCCCTATTATGAACTGGAGAGTGTGCACTGTCCT
GGCCTCAACTTGCTGGATATTTAGCTTTCTCTTGGCTCTGGTCCATATTACTCTTATTCTGA
GGCTGCCTTTTTGTGGCCCAAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC
AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTTATTTGCGGGTTCTGCGTTCA
TCTTAGTGCGGGCCGCTCTGCCTGGTGCTGGTCTCTACTTGCACATCCTGGTGGCCATCTTG
25 AGGATCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG
TGGTGGGGCTTTTCTTTGGCAGCGCCATTGT CATGTACATGGCCCCCAAGTCAAGCCATTC
TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC
CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCCTTTGGAAA
CAGAGATCAATGTGA (SEQ ID NO: 484).

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AOLFR259 sequences:

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL
AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVVMYSYDRFVAICHPL
HYTVIMNWRVCTVLAITSWACGFSALINLILLRLPFCGPQEVNHFFGEILSVLKLACADTWIN
35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY
LVPDNSQRQKQKILTLFYSLFNPLLNPLIYSLRNAQVKGALYRALQKKRTM (SEQ ID NO:
485).

40 ATGGGGGACAACCAATCACGGGTACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG
GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAAA
TGGCATGATCTTGGGGCTCATCTGTCTGGATCCAGACTGCGCACCCCCATGTACTTCTTCC
TGTCACACTTGGCCGTCAATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA
AAACCTAGTGAAACACAAAAAACTATCTCGTTCATCTCTTG CATTATGCAGATGGCTTTG
TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCCTATGACAGATTGT
45 GGCGATCTGCCATCCCCTGCATTACACTGTCATCATGAACTGGAGAGTGTGCACAGTACTG
GCTATTACTTCCTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG
GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTTCTGTCTGTCCTC
AAACTGGCCTGTGCAGACACCTGGATTAATGAAATTTTTGTCTTTGCTGGTGGTGTGTTTG
TCTTAGTCGGGCCCCCTTTCTTGATGCTGATCTCTACATGCGCATCCTCTTGGCCATCCTG
50 AAGATCCAGTCAAAGGAGGGCCGAAAAAGCCTTTTCCACCTGCTCCTCCACCTCTGTG
TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG
ACAGAAGCAGCAGAAAATTCTCACCTGTTTTACAGCCTTTTCAACCCATTGCTGAACCCC
CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCCTTATACAGAGCACTGCAGAAA
AAGAGGACCATGTGA (SEQ ID NO: 486).

55

AOLFR24B sequences:

MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM
LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMETVLLVVMAYDRFVAICNP
LQYTMILTNNKTISILASVVVGRNLVLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN
5 IYGLMVISYIIVDVILIASSYVLILRAVFLPSQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH
RFGQNIPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCCTTCTTCTCCTGCTAGGAATACCAGG
ACTGGACACTTTACATATCTGGATTCTTTTCCCATCTGTATTGTGTACCTGATTGCCATTG
10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATGTT
CTACTTCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA
TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT
GTTCTTTATTACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC
GCTTTGTTGCCATCTGCAACCCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG
15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA
TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG
TCTGGCCGGGTTGGCCTGTGCACCCATTAAGATCAACATAATCTATGGGCTCATGGTGATT
TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT
TTTTCGCCTTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT
20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTCTTTTATGACACATCGTTTTGGCCAA
AACATTCCTCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCCACCTGCCCT
TAACCTGTCAATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTGTGAAAATATTT
GTACAGAAAGAATAA (SEQ ID NO: 488)

AOLFR33B sequences:

MLHTNNTQFHPSTFLVVGVPGLDVHVWIGFPFFAVYLTALLGNIILFVIQTEQSLHQPMFYFL
AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTIHICTGLESVVLTVTGIDRYIAICNP
LRYSMILTNNKVIAILGIVHVRTLVFVTPFTFLTLRLPFCGVRIIPHTYCEHMGAKLACASINVIY
GLIAFSVGYIDISVIGFSYVQILRAVFHLPAPWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF
30 GHNIPHYIHILLANLYVVVPPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ
(SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCTTCCACCTTCTCCTCGTAGTGGGGGTCCCAG
GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT
35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG
TTTTACTTCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA
AGATGCTGGGAATTTTCTGGTTTAATCTTGGAGAGATTGCATTTGGTGCCTGCATCACACA
GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA
GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA
40 TAGCCATTCTGGGCATAGTCATCATTTGTCAGGACTTTGGTATTTGTGACTCCATTACATTT
CTCACCTGAGATTGCCTTCTGTGGTGTCCGGATTATCCCTCATACCTATTGTGAACACAT
GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA
GTGGGATACATTGACATTTCTGTGATTGGATTTTCTCATGTCCAGATCCTCCGAGCTGTCTT
CCATCTCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT
45 GTTATGTTGGCTTTTCTACCTGCCAGCCCTCTTTTCTTCATGACACACCGCTTTGGCCACAA
CATCCCTCATTACATCCACATTCTTCTGGCCAATCTGTATGTGGTTTTTCCCCCTGCTCTTA
ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA
ACCCTAAAAGCTTTTGGCATTTTGACCCCAAGAGGATCTTCCACAACAATTACAGTTAGACA
ATAA (SEQ ID NO: 490)

50

AOLFR112B sequences:

MKNKTVLTEFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILTLTLLDSHLQTPMYFFLRNFSF
LEISFTNIFIPRVLSITTNKNSISFAGCFTQYFFAMFLGATEFYLLAAMSVDYVAICKPLHYTTI
MSSRICIQLIFCSWLGLMAIPTITLMSQQDFCASRNLNHYFCDYEPLLELSCSDTSLIEKVVFL
55 VASVTLVVTLLVLVLSYAFIHKILKLPAAQQRKAFSTCSSHMIVISLSYGSCMFMYNPSAKEG
DTFNKGVALLITSVAPLLNPFYITLRNQVKQPFKDMVKKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC
TCCAGGTGGCAGTTTTACCTTTCTTTTCCTTGGCTATTTACTCAGCATCCTTGGAATCTG
5 ACTATCCTCATCCTCACCTTGCTGGACTCCCACCTTCAGACTCCCATGTATTTCTTTCTCCG
GAACTTCTCCTTCTTGGAATTTCTTTCACAAACATCTTCATTCCAAGGGTCTGATTAGCA
TCACAACAGGGAACAAGAGTATCAGCTTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT
GTTCCCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC
ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT
TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA
10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA
CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCTTTCTTGTGGCATCTGTGACCC
TGGTGGTCACTCTGGTGCTAGTGATTCTCTCCTATGCATTCATTATCAAGACTATTCTGAAG
CTCCCCTCTGCCCAACAAAGGACAAAAGCCTTTTCCACATGTTCTTCCCACATGATTGTCAT
CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT
15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT
TTACACCCTAAGGAACCAACAGGTAACAAACCCTTCAAGGATATGGTCAAAAAGCTTCT
GAATCTTTAA (SEQ ID NO: 492)

AOLFR130B sequences:

20 MEGKNQTAPSEFIILGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL
ALIDICYTTTNVPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR
YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFLHLPFCGNNQINYFFCDIPLLILSCGDTSLNE
LALLSIGILISWTPFLCIILSYLYIISTILRISSEGRHKAFSTCASHLLIVILYYSIAIFTYVRPISSYS
LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA
ATGAATTGCAGTATTTACTCTTCACCATCTTCTTTCTGACCTACATATGCACTTTAGGAGGC
AATGTTTTTATCATTGTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT
CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG
30 GTGCATCTTCTGTGAGAGAAGAAAATCATTTCCTATGGAGGCTGTGTGACCCAGCTCTTTG
CATTCATTTTCTTTGTTGGCTCAGAGTGTCTCCTCCTGGCAGCAATGGCATATGATCGATAT
ATTGCTATCTGTAAGCCGTTAAGGTACTCATTATTATGAACAAGGCCCTGTGCAGCTGGT
TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT
CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTCTTCTGTGACATACCTCCCTTGC
35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAAGTGGCTTTGCTGTCCATTGGGATCCTC
ATAAGCTGGACTCCTTTCTGTGCATCATCCTTTCTACCTTTACATCATCTCCACCATCCT
GAGGATCCGTTCCCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCACCTGCTC
ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC
TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTACACCCATGCTGAATCCT
40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG
TGGCAGCCACCAGTTTTCTCTTCTGATATATAA (SEQ ID NO: 494)

AOLFR142B sequences:

MARKDMAHINCTQATEFILVGLTDHQELKMPLFVLFLSIYLFVVGNLGLILLIRADTSLNTPM
45 YFFLSNLA FVDFCYSSVITPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLLASMAYDRY
VAICNPLLYMVVMTPGICQLVAVPYSYSFLMALFHTILTFRLSYCHSNIVNHFYCDMPLLRL
TCSDFTRFKQLWIFACAGIMFISSLLIVFVSYMFIIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG
TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIINKN (SEQ ID NO:
495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG
GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC
TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA
CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTTCTGTTACTCTTCTGTCATT
55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG
CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAACCCTCTATTGTATATGGTTGTAATGACTCCAG
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTAC
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTTCTATTGTGA
 5 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT
 GCCTGTGCTGGTATCATGTTTCATTTCCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC
 ATTTCTGCCATCCTGAGGATGCATTACAGTCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC
 10 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA
 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

AOLFR171C sequences:

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL
 AFVDLCYSSAITPKMMVNFVVERNITIPFHACATQLGCFLTFMITECFLLASMAYDCYVAICSPL
 15 HYSTLMSRRVCIQLVAVPYIYSFLVALFHTVITFRLTYCGPNLINHFYCDLPLALSCSDTHMK
 EILIFAFAGFDMISSSSVLTSYIFIIAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLQPKS
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCATTCTGAAAGGAATTACCAACCGGC
 CAGAGCTTCAGGCCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG
 GTGAATTTTGTGTGGAACGCAACACCATTCCCTTCCATGCTTGTGCAACCCAACCTGGGTT
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCCTTCTAGCCTCCATGGCCTACGATTGCTAT
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC
 TGGTGGCAGTTCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTTC
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTTCATTGTGATGACCTCCCCTTCTT
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATTCTGATATTTGCCTTTGCTGGCTTT
 30 GATATGATCTCTTCTTCCATTGTCCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCACCTGTGGTCCCATATGGTGA
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG
 35 GTTGTGAAAACCTTACAGATATTAACATTTTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:
 498)

AOLFR225B sequences:

MKNRTMFGEFILLGLTNQPELQVMIFIFLFLTYMLSILGNLTIITLTLDDPHLQTPMYFFLRNFSF
 40 LEISFTSIFIPRLTSMTTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAICKPLHYLTI
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI
 LLAVVTLMVTLVLVTLSTYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE
 GGA FNKGIAVLITSVTPLLNPFYITLRNQVKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC
 TCCAAGTGATGATATTCATCTTTCTGTTCCCTACCTACATGCTAAGTATCCTAGGAAATCTG
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCTCCG
 GAATTTCTCCTTCTTAGAAATTTCTTCCATCCATTTTTATTCCCAGATTTCTGACCAGCA
 TGACAACAGGAAATAAAGTTATCAGCTTTGCTGGCTGCTTGACTCAGTATTTTTTGTCTAT
 50 ATTTCTTGGAGCTACCGAGTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA
 TCTGCAAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT
 CTGCTCCTGGTTGGGGGGATTCCTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGAGCT
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA
 TCCCTTCTGCCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCTCCCATGATTGTCTATC

TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG
CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA
TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG
AAACTTTAA (SEQ ID NO: 500)

5

AOLFR274B sequences:

MEFVFLAYPSCPELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV
VVPFILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMAYDRYVAICHPLQYPLLMTLTL
CVHLVVASVISGLFSLQLVAFISLPFCQAQGIEHFFCDVPPVMHVCAQSHIHEQSVLVAAIL
10 AIAVPFFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVLLQYGCCAFMYLCPSSSYNPKQ
DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTCTGGCCTATCCCTCCTGCCAGAACTGCATATTCTGTCCTTCCTTGG
GGTCAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC
15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA
TATGCTACACTGCAGTGGTGGTGCCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC
CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGTGAT
TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTTGCCACCCGTTGCAGTA
CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTTGTGGCATCAGTCATCAGTGGTC
20 TGTTCTGTCTTACAACCTGGTGGCCTTCATCTTCTCTGCCATTCTGCCAGGCTCAGGGC
ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT
TCATGAGCAGTCAGTGTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC
ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC
ACCGGGCCTTCTCCACCTGCTCTTCCCACCTCACTGTGGTGTGCTGCAGTATGGCTGCTGT
25 GCCTTCATGTACCTGTGCCCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC
TGGTGTACACATTGGGAACCCCACTGCTCAACCCACTTATCTATGCCCTGAGGAACAGTGA
GATGAAAGGGGCCGTAGGGAGAGTTCTTACCAGGAACTGCCTTTCCAGAACAGCTAG
(SEQ ID NO: 502)

30 **AOLFR276B sequences:**

MGGFGTNISSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIIKEEQSLHQPMYYFLS
LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFHDHYVAICNP
LRYATVLT DVRVAHNGISIVIRSF CMVFPLPFLKRLPFCKASVVL AHSYCLHADLIRLPWGD
TINS MYGLFIVISAFGVDSL LILLSYVLILHSVLAIASRGERLKT LNTCVSHIYAVLIFYVPMVSVS
35 MVHRFGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG
AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCCCTT
CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGACCAGCCAATG
40 TACTACTTCTGTCTCTTTTCTGTTAATGACCTGGGTGTGCTCTTTTCTACATTGCCCACT
GTACTGGCTGCTGTGTGTTTTATGCCCCAGAGACAACCTTTTGATGCCTGCCTGGCCCA
TGTTCTTCATCCACTTTTCTCCTGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTTGAC
CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG
CCCACAATGGCATATCCATTGTGATCCGCAGCTTCTGCATGGTATTCCCACTTCCCTTCCTC
45 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCTACTGTCTGCATG
CAGACCTGATTGCGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCT
TGTCATCTCTGCCTTTGGTGTAGATTCACTGCTCATCCTCCTCTCCTATGTGCTCATTCTAC
ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC
ACATATCTATGCAGTGTGATCTTCTATGTGCCTATGGTTAGTGTGTCATGGTTTCATCGAT
50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT
ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

AOLFR311B sequences:

MDWENCSSLTDFLLGITNNPEMKVTLFAVFLAVYIINF SANLGMIVLIRMDYQLHTPMYFFLS
55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLLSVMAFDYKAINP
LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHSAEGRFKALSTCTSHLSAVAIFQGTLLFMYFRP
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTATTTTTTCTCTTGGGAATTACCAATAACCC
AGAGATGAAAGTGACCCTATTTGCTGTATTCTTGGCTGTTTATATCATTAATTTCTCAGCAA
ATCTTGGAATGATAGTTTTAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCCAAGATGCTGG
TAGATCTACTTGCCAAGAACAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTTCTTGGT
CTTCTGTATCTTTGCGAGATTCTGAGTGTCTACTGCTGTGATGATGGCCTTTGATCGGTACA
10 AGGCCATCATCAACCCCCTGCTCTATACAGTCAACATGTCTAGCAGAGTGTGCTATCTACT
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTATTACCGTCTTTGGTTTTA
TTGAACTGAGTACCATTTTCAAGAGTTTTTCAATTTCTTATTGTTATATCATCCTATCAGTCTTG
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTCTACATGCACTTCCCACTTATCTG
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTTATGTATTTCCGGCCAAGTTCTTCCTATTCT
CTAGATCAAGATAAAATGACCTCATTGTTTTACACCCTTGTTGGTTCCCATGTTGAACCCCT
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAAGTAAAAATAAAAT
TTTATTTTAA (SEQ ID NO: 506)

20

AOLFR314 sequences:

MEVKNCCMVTEFILLGIPHTEGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG
NLSVDFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFFHFLGSIIEFLFTVMAYDRFTAICY
PLRYTVIMNPRICVALAVGTWLLGCIHSSILTSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL
25 AQRVSFTNVGLISLVCFLLILLSYTRITISILSIRTTEGRRRAFSTCSAHLIAILCAYGPIITVYLQPT
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKTALKTILHRTGHVPES (SEQ ID NO: 507)

ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCACACACACA
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG
30 AAATGTGTCTATCCTTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTCT
TCCTGGGAAACTTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGAAGTGTGCTGCCCCAAATGCT
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTGTTACGGTGATGGCCTATGACCGCTTC
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATCCAGTATCTTGACCTCCCTCACCTTC
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCCAGCACTGTT
GCCCTTGGCCTGTGCTGACACATCCTTAGCCCAGAGGGTGAGCTTCACCAACGTTGGCCTC
ATATCTCTTGTCTGCTTTCTGCTAATTCTTTTATCCTACACTAGAATCACAATATCTATCTT
AAGCATTCGTACAAGTGAAGGGCCGTCGCCGTGCCTTCTCCACCTGCAGTGCTCACCTCATT
40 GCCATCCTCTGTGCCTATGGGCCCATCATCACTGTCTACCTGCAGCCCACACCCAACCCCA
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

45 **AOLFR324B sequences:**

MPIANDTQFHTSSFLLLGPGLLEDVHIWIGFPFFSVYLIALLGNAAIFFVIQTEQSLHEPMYYCLA
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFFTVMESIVLVAMAFDRYIAICKPL
WYTMILTSKIISLIAGIAVLRSLYMPIVLVLLLRPLFCGHRHPIPTYCEHMGARLACASIKVNIM
FGLGSISLLLLDVLLILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH
50 DIPQYIHIFLANLYVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCATACTTCTTCATTCCTACTGCTGGGTATCCCAGG
GCTAGAAGATGTGCACATCTGGATTGGATTCCCTTTTTTCTCTGTGTATCTTATTGCACTCC
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCACAAA
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTTCTCAGA

TGTTCCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC
 CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA
 GCCTCATTGCAGGCATTGCTGTCTGAGGAGCTTGACATGGTCATTCCACTGGTGTCTCT
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG
 5 GCATTGCCCCTGTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT
 TTCTCTCTTGTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT
 CTCTGCTGCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT
 GATATTCCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTTGTTCCTCCCACCCT
 10 CAATCCTGTAATCTATGGGGTCAGAACCAAACATATTAGGGAGACAGTGCTGAGGATTTTC
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

AOLFR328 sequences:

15 MALGNHSTITEFLLLGLSADPNIRALLFVFLGIYLLTIMENLMLLLVRADSCLHKPMYFFLSH
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVVTAGTEACLLSGMAYDRHAAIRRP
 LLYGQIMGKQLYMHVWGSWGLGFLDALINVLLAVNMVFEAKIIHHYSYEMPSLLPLSCSDI
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTILSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL
 MPNSGSPIELIFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCTGGGCTGTCTGCCGACC
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTCTGCGGGATTACCTCCTGACCATAATGGA
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT
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